



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 131428

TO: Rosanne Kosson
Location: rem/3b84/3e71
Art Unit: 1651
September 8, 2004

Case Serial Number: 10/619149

From: P. Sheppard
Location: Remsen Building
Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes

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STIC-Biotech/ChemLib

131 428

my

From: Kosson, Rosanne
Sent: Tuesday, August 31, 2004 5:59 PM
To: STIC-Biotech/ChemLib
Cc: Prats, Frank
Subject: request for sequence search

Could you search a sequence for me- application no. 10/619,149, SEQ ID NO: 1, which is a protein sequence (human PEDF)? Please let me know if you need any additional info for the conducting the searches. Thanks!!!

Rosanne Kosson
Patent Examiner, AU 1651
REM 3B84
571-272-2923
rosanne.kosson@uspto.gov

3E71

619
103-1-023
RECEIVED

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence :# _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: September 1, 2004, 10:58:23, Search time 125 Seconds
(without alignments)
944.839 Million cell updates/sec

Title: US-10-619-149-1
Perfect score: 2131
Sequence: 1 MQALVLLCIGALLGHSSCO.....RDTDTGALLFIGKILDPGRP 418

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2125	99.7	418	2 AAR90287	Aar90287 Pigment e
2	2125	99.7	418	4 AAE10306	Aae10306 Human pig
3	2125	99.7	418	5 ABB81091	Abb81091 Human pig
4	2125	99.7	418	6 AAE38136	Aae38136 Human ret
5	2125	99.7	418	7 ABUI10031	Abui10031 Human pig
6	2106	98.8	418	2 AAR44800	Aar44800 Sequence
7	2106	98.8	418	6 ABR58379	Abr58379 Human NOV
8	2097	98.4	418	6 ABR72122	Abg72122 Human pig
9	2097	98.4	418	7 ADB99089	Adb99089 Human ret
10	1904	89.3	379	2 AAR90288	Aar90288 Modified
11	1870	87.8	379	6 ABR72123	Abg72123 Truncated
12	1870	87.8	379	7 ADB99090	Adb99090 Human ret
13	1789	84.0	418	5 ABB57391	Abb57391 Rat mucoc
14	1784	83.7	362	2 AAU87364	Aau87364 Amino aci
15	1784	83.7	362	4 AAU86652	Aau86652 Human ant
16	1784	83.7	362	5 ABB08433	Abb08433 SLED poly
17	1784	83.7	362	5 ABB04587	Abb04587 Human ant
18	1651	77.5	362	4 AAE10305	Aae10305 Human pig
19	499	23.4	125	4 AAB87625	Aab87625 Bovine ma
20	472	22.1	111	3 AAG031717	Aag031717 Human sec
21	464.5	21.8	491	3 AAY59193	Aay59193 Mouse alp
22	458.5	21.5	124	4 AAO07150	Aao07150 Human pol
23	457.5	21.5	491	3 AAY59192	Aay59192 Bovine al
24	457	21.4	490	2 AAR04252	Aar04252 Amino aci
25	456.5	21.4	488	3 AAY59191	Aay59191 Human alp

26	456.5	21.4	491	2	AAR13860	Aar13860 Human alp
27	456	21.4	492	1	AAP90486	Aap90486 Human alp
28	455	21.4	452	1	AAP90534	Aap90534 Peptide s
29	455	21.4	464	2	AAR05411	Aar05411 Pro-type
30	450.5	21.1	744	1	AAP81006	Aap81006 Alpha-2-p
31	444	20.8	413	5	ABG91415	Abg91415 Primate L
32	432.5	20.3	503	5	AAY99881	Aay99881 SLAP1 fus
33	432	20.3	418	1	AAP50021	Aap50021 Sequence
34	430	20.2	417	3	AAB36101	Aab36101 Human alp
35	430	20.2	417	3	AAB26705	Aab26705 Human alp
36	430	20.2	417	7	ADE34542	Ade34542 Human alp
37	430	20.2	418	2	AAR22931	Aar22931 Alpha-1-a
38	429.5	20.2	413	2	AAW23138	Aaw23138 Protease
39	429	20.1	418	6	ABR48498	Abr48498 Human Alp
40	428	20.1	418	7	ADE60631	Ade60631 Human Pro
41	428	20.1	418	7	ADD45920	Add45920 Human Pro
42	427	20.0	394	2	AAP67362	Aap67362 Alpha-1-a
43	427	20.0	418	1	AAP40133	Aap40133 Sequence
44	427	20.0	418	1	AAP94664	Aap94664 Predomina
45	427	20.0	418	2	AAY26925	Aay26925 Human alp

ALIGNMENTS

RESULT 1
AAR90287
ID AAR90287 standard; protein; 418 AA.
XX
AC AAR90287;
XX
DT 16-JAN-1997 (first entry)
XX
DE Pigment epithelium-derived factor.
XX
KW Pigment epithelium-derived factor; PEDF; neuronal cells; neurons;
glial cells; gliastatic; gliosis; central nervous system; CNS;
neurodegenerative disease; injury; neurotrophic; brain cells;
Parkinson's disease; photoreceptor cells; retina; inhibition;
proliferation; immunoassay; antibody; ageing; degenerative disease.
XX
OS Homo sapiens.
XX
PN WO9533480-A1.
XX
PD 14-DEC-1995.
XX
PF 06-JUN-1995; 95WO-US007201.
XX
PR 07-JUN-1994; 94US-00257963.
PR 30-DEC-1994; 94US-00367841.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Chader GJ, Becerra SP, Schwartz JP, Taniwaki T;
XX
DR WPI; 1996-039966/04.
DR N-PSDB; AAT11658.
XX
PT Use of pigment epithelium derived factor - for enhancing neuronal cell
survival and inhibiting glial cell proliferation, useful, e.g. in CNS
cell culture or to treat neuro-degenerative diseases.
XX
PS Disclosure; Page 64-65; 151pp; English.
XX
CC Pigment epithelium-derived factor (PEDF) has both neurotrophic and
gliastatic activity, making it useful in cases where neurons die quickly
and glia tend to proliferate (gliosis), e.g. in CNS cell culture, in
neurodegenerative diseases and in CNS injury. The neurotrophic effect
of PEDF is especially useful for enhancing survival of neuronal cell
cultures intended for use in transplantation. These include cultures of
human foetal brain cells and neural retina and photoreceptor cells. The
gliastatic activity of PEDF can be applied to inhibiting glial cell

CC proliferation in certain tumours. Antibodies directed against PEDF can be
 CC used for inhibiting PEDF activity or in an immunoassay for determining
 CC levels of PEDF in fluid, cellular or tissue samples e.g for determining
 CC ageing and/or other degenerative diseases
 XX
 SQ Sequence 418 AA;

Query Match 99.7%; Score 2125; DB 2; Length 418;
 Best Local Similarity 99.5%; Pred. No. 3.3e-189;
 Matches 416; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQALVLLLCIGALLGHSSCCNPASPPEEGSPDPDSTGALVEEDPFFKVPVVKLA AAVSN 60
 DB 1 MQALVLLLCIGALLGHSSCCNPASPPEEGSPDPDSTGALVEEDPFFKVPVVKLA AAVSN 60

QY 61 FGVDLYVRSSMSTTNVLLSPVATALSALSGAEQRTESIHRALYYDLISSPDING 120
 DB 61 FGVDLYVRSSMSTTNVLLSPVATALSALSGADETESIHRALYYDLISSPDING 120

QY 121 TYKELDTVTAPQNLKASRIKSFVAPLEKSYGTRPRVLTGNPRLDLQEI 180
 DB 121 TYKELDTVTAPQNLKASRIKSFVAPLEKSYGTRPRVLTGNPRLDLQEI 180

QY 181 NNWQAQMGKGLARSTKEIPDEISILLGVAFHGQVTKFDSRKTSLEDFYLDERTVR 240
 DB 181 NNWQAQMGKGLARSTKEIPDEISILLGVAFHGQVTKFDSRKTSLEDFYLDERTVR 240

QY 241 VPMMSDPKAVLRGLDSDLCKIAQLPLTGSMIIFFLPKVTQNTLIEESITSEFIHD 300
 DB 241 VPMMSDPKAVLRGLDSDLCKIAQLPLTGSMIIFFLPKVTQNTLIEESITSEFIHD 300

QY 301 IDRELKTVQAVLTPVKLKSVEGEVTKSLQEMKLSLFDSPFSKITGPKIKLTQVEHRA 360
 DB 301 IDRELKTVQAVLTPVKLKSVEGEVTKSLQEMKLSLFDSPFSKITGPKIKLTQVEHRA 360

QY 361 GFENWEDGAGTTSPGLOPAHLTPFLDYHLNQPFIFVLRDTDTGALLFGKILDPGPG 418
 DB 361 GFENWEDGAGTTSPGLOPAHLTPFLDYHLNQPFIFVLRDTDTGALLFGKILDPGPG 418

RESULT 2
 AAEL0306
 ID AAEL0306 standard; protein; 418 AA.
 XX
 AC AAEL0306;
 XX
 DT 10-DEC-2001 (first entry)
 XX
 DE Human pigment epithelium derived growth factor (PEDF).
 XX
 KW Human; pigment epithelium derived growth factor; PEDF; angiogenesis;
 KW tumour; benign neoplasia; ischaemic retinopathy; macular degeneration;
 KW scleroderma; infection; cat scratch disease; muscle active general;
 KW bacterial ulceration; diabetic retinopathy; neuroblastoma; haemangioma;
 KW muscle disease; myocardial angiogenesis; arthritis; haemophilic joint;
 KW Osler-Webber Syndrome; plaque neovascularisation; telangiectasia;
 KW angiofibroma; wound granularisation; cytostatic; therapy; psoriasis;
 KW antiinflammatory; antipsoriatic; antiviral; antidiabetic; cardiac.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 318
 FT /note= "Encoded by AGG"
 XX
 XX W0200162725-A2.
 XX
 XX 30-AUG-2001.
 XX
 XX 22-FEB-2001; 2001WO-US005915.
 XX
 XX 23-FEB-2000; 2000US-00511683.
 XX
 XX 23-JUN-2000; 2000US-00603478.
 PR

XX (NOUN) UNIV NORTHWESTERN.
 PA Bouck NP, Dawson DW, Gillis PR, Crawford SE, Stellmach VM;
 PI Volpert O;
 XX WPI: 2001-582032/65.
 DR N-PSDB; AAD17438.
 XX
 PT Inhibiting angiogenesis within a tissue in a mammal, comprises providing
 PT exogenous pigment epithelium derived growth factor (PEDF) systemically to
 PT the mammal, useful for treating ischemic retinopathy, macular
 PT degeneration and psoriasis.
 XX
 PS Claim 20; Page 96-98; 100pp; English.

XX The invention relates to a method of inhibiting angiogenesis within a
 CC tissue by providing exogenous pigment epithelium derived growth factor
 CC (PEDF) to cells associated with the tissue. The presence of exogenous
 CC PEDF inhibits angiogenesis within the tissue, in part by interfering with
 CC the ability of vascular endothelia to expand within the tissue. The
 CC invention also provides a method for determining the severity of a tumour
 CC by assaying for the presence of PEDF within the tumour. PEDF inhibits
 CC angiogenesis within the tissue and is useful for treating a benign
 CC neoplasia of a nasal polyp or the prostate gland, ischaemic retinopathy
 CC and macular degeneration. PEDF is useful for treating diseases and
 CC disorders such as psoriasis, scleroderma, tumours of the skin,
 CC neovascularisation as a consequence of infection (e.g., cat scratch
 CC disease, bacterial ulceration, etc.), diabetic retinopathy, a tumour
 CC (e.g., a benign or cancerous growth), and childhood tumours (including,
 CC but not limited to, neuroblastoma). PEDF can also be used for treating
 CC disorders of blood vessels (e.g., haemangiomas), muscle diseases (e.g.,
 CC myocardial angiogenesis or angiogenesis within smooth muscles), joints
 CC (e.g., arthritis, haemophilic joints, etc.), and other disorders
 CC associated with angiogenesis (e.g., Osler-Webber Syndrome, plaque
 CC neovascularisation, telangiectasia, angiofibroma, wound granularisation,
 CC etc.). PEDF can also retard the growth of existing tumours. The present
 CC sequence is human PEDF protein. Note: this sequence SEQ.ID.NO.1 is slated
 CC to be similar to the sequence shown in Fig 6A (AAEL0305). However this
 CC sequence differs at several locations from the sequence shown in Fig 6A
 XX
 SQ Sequence 418 AA;

Query Match 99.7%; Score 2125; DB 4; Length 418;
 Best Local Similarity 99.5%; Pred. No. 3.3e-189;
 Matches 416; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQALVLLLCIGALLGHSSCCNPASPPEEGSPDPDSTGALVEEDPFFKVPVVKLA AAVSN 60
 DB 1 MQALVLLLCIGALLGHSSCCNPASPPEEGSPDPDSTGALVEEDPFFKVPVVKLA AAVSN 60

QY 61 FGVDLYVRSSMSTTNVLLSPVATALSALSGAEQRTESIHRALYYDLISSPDING 120
 DB 61 FGVDLYVRSSMSTTNVLLSPVATALSALSGADETESIHRALYYDLISSPDING 120

QY 121 TYKELDTVTAPQNLKASRIKSFVAPLEKSYGTRPRVLTGNPRLDLQEI 180
 DB 121 TYKELDTVTAPQNLKASRIKSFVAPLEKSYGTRPRVLTGNPRLDLQEI 180

QY 181 NNWQAQMGKGLARSTKEIPDEISILLGVAFHGQVTKFDSRKTSLEDFYLDERTVR 240
 DB 181 NNWQAQMGKGLARSTKEIPDEISILLGVAFHGQVTKFDSRKTSLEDFYLDERTVR 240

QY 241 VPMMSDPKAVLRGLDSDLCKIAQLPLTGSMIIFFLPKVTQNTLIEESITSEFIHD 300
 DB 241 VPMMSDPKAVLRGLDSDLCKIAQLPLTGSMIIFFLPKVTQNTLIEESITSEFIHD 300

QY 301 IDRELKTVQAVLTPVKLKSVEGEVTKSLQEMKLSLFDSPFSKITGPKIKLTQVEHRA 360
 DB 301 IDRELKTVQAVLTPVKLKSVEGEVTKSLQEMKLSLFDSPFSKITGPKIKLTQVEHRA 360

QY 361 GFENWEDGAGTTSPGLOPAHLTPFLDYHLNQPFIFVLRDTDTGALLFGKILDPGPG 418
 DB 361 GFENWEDGAGTTSPGLOPAHLTPFLDYHLNQPFIFVLRDTDTGALLFGKILDPGPG 418

Db 361 GFEWNEGAGTTPSGQLQPAHLTFPLDYHLNQPFIFVLRTDTGALLFIGKILDRGP 418

RESULT 3

ABB81091

ID ABB81091 standard; protein; 418 AA.

XX AC ABB81091;

XX DT 05-NOV-2002 (first entry)

XX DE Human pigment epithelium-derived factor (PEDF) sequence.

XX KW PEDF; choroidal neovascularization; photoactive; ocular; antidiabetic;

XX KW ophthalmological; photodynamic therapy; retina; angiogenic; human;

XX KW pigment epithelium-derived factor.

XX OS Homo sapiens.

XX FN WO200258730-A2.

XX PD 01-AUG-2002.

XX PF 26-OCT-2001; 2001WO-US051062.

XX PR 01-NOV-2000; 2000US-0244850P.

XX PA (ALLR) ALLERGAN SALES INC.

XX PI Wheeler LA, De Vries GW;

XX DR WPI; 2002-619144/66.

XX PT Treatment useful for choroidal neovascularization involves combining

XX PT photodynamic therapy with the administration of an antiangiogenic

XX PT compound.

XX PS Disclosure; Page 4; 33pp; English.

XX CC The invention relates to the treatment of choroidal neovascularization

XX CC that involves administering a photoactive compound to localize the

XX CC affected target ocular tissue, irradiating the tissue with light emitted

XX CC from a laser at a wavelength for absorption by the photoactive compound

XX CC and then administering an antiangiogenic compound to inhibit recurrence

XX CC of neovascularization. The method is useful for the treatment of

XX CC choroidal neovascularization and to protect ocular neural tissue from

XX CC damage caused by photodynamic therapy; and also for the treatment of

XX CC diabetic retinopathy. The method is more selective closure of blood

XX CC vessels, in order to preserve the overlying neurosensory retina. This

XX CC method is safer than photocoagulation. The present sequence represents

XX CC the human pigment epithelium-derived factor (PEDF), used as the

XX CC antiangiogenic compound in the method of the invention

XX SQ Sequence 418 AA;

Query Match 99.7%; Score 2125; DB 5; Length 418;

Best Local Similarity 99.5%; Pred. No. 3.3e-189;

Matches 416; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQALVLLLCIGALLGHSSCONPASPPEGSPDPDSTGALVEEDPFFKVPVKNKLAASN 60

Db 1 MQALVLLLCIGALLGHSSCONPASPPEGSPDPDSTGALVEEDPFFKVPVKNKLAASN 60

Qy 61 FGVDLYRVRSSMPTTNVLLSPLSVATLSALSLCAQRTESIHRALYYDLISSPDING 120

Db 61 FGVDLYRVRSSMPTTNVLLSPLSVATLSALSLCAQRTESIHRALYYDLISSPDING 120

Qy 121 TYKELLDTVTAPQKNLKSASRIVFEKKLRIKSSFVAPLEKSYGTRPVLIGNPRLDLOEI 180

Db 121 TYKELLDTVTAPQKNLKSASRIVFEKKLRIKSSFVAPLEKSYGTRPVLIGNPRLDLOEI 180

Qy 181 NNWQAOQMGKGLARSTKEIPDEISILLGVAFHKGQWTKFSDSKTSIEDFYLDERTVR 240

Db 181 NNWQAOQMGKGLARSTKEIPDEISILLGVAFHKGQWTKFSDSKTSIEDFYLDERTVR 240

Qy 241 VPMMSDPKAVLRGLDSDLSCKIAQLPLTGSMSIIFFLPLKVTQNTLTIIEESLTSEFIHD 300

Db 241 VPMMSDPKAVLRGLDSDLSCKIAQLPLTGSMSIIFFLPLKVTQNTLTIIEESLTSEFIHD 300

Qy 301 IDRELKTVOAVLTVPKLSYEGEVTKSLQENKLSLQSLDPSDFSKITGKPIKLTQVEHRA 360

Db 301 IDRELKTVOAVLTVPKLSYEGEVTKSLQENKLSLQSLDPSDFSKITGKPIKLTQVEHRA 360

Qy 361 GFEWNEGAGTTPSGQLQPAHLTFPLDYHLNQPFIFVLRTDTGALLFIGKILDRGP 418

Db 361 GFEWNEGAGTTPSGQLQPAHLTFPLDYHLNQPFIFVLRTDTGALLFIGKILDRGP 418

RESULT 4

AAE38136

ID AAE38136 standard; protein; 418 AA.

XX AC AAE38136;

XX DT 20-NOV-2003 (first entry)

XX DE Human retinal pigment epithelium derived factor (PEDF).

XX KW Human; pigment epithelium derived factor; PEDF; diabetic retinopathy;

XX KW anti-angiogenic; neurotrophic; gliastatic; therapy; cell proliferation;

XX KW age-related macular degeneration; neuronal disease; retinal detachment;

XX KW tumour.

XX OS Homo sapiens.

XX FN WO2003059248-A2.

XX PD 24-JUL-2003.

XX PF 02-JAN-2003; 2003WO-IL000007.

XX PR 03-JAN-2002; 2002IL-00147444.

XX PA (YEDA) YEDA RES & DEV CO LTD.

XX PI Shaltiel S, Schwartz I;

XX DR WPI; 2003-598472/56.

XX PT New isolated pigment epithelium derived factor (PEDF) or its fragment or

XX PT derivative isolated from plasma or its salt, useful for preparing a

XX PT composition for treating neuronal or angiogenesis-related disease, e.g.,

XX PT choroidal tumors.

XX PS Disclosure; Page 57-58; 60pp; English.

XX CC The invention relates to pigment epithelium derived factor (PEDF)

XX CC comprising inhibitory activity of endothelial cell proliferation, anti-

XX CC angiogenic activity, neurotrophic activity, neurotrophic activity or

XX CC gliastatic activity. The PEDF is useful for preparing a composition for

XX CC treating neuronal disease or angiogenesis-related disease, e.g., age-

XX CC related macular degeneration, diabetic retinopathy, retinal detachment,

XX CC retinal tumours and choroidal tumours. The present sequence is human

XX CC retinal PEDF protein

XX SQ Sequence 418 AA;

Query Match 99.7%; Score 2125; DB 6; Length 418;

Best Local Similarity 99.5%; Pred. No. 3.3e-189;

Matches 416; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQALVLLLCIGALLGHSSCONPASPPEGSPDPDSTGALVEEDPFFKVPVKNKLAASN 60

Db 1 MQALVLLLCIGALLGHSSCONPASPPEGSPDPDSTGALVEEDPFFKVPVKNKLAASN 60

Qy 61 FGVDLYRVRSSMPTTNVLLSPLSVATLSALSLCAQRTESIHRALYYDLISSPDING 120

```

Db 61 FGYDLVRSSMSPTTNVLLSPLSVATALSALSGADERTESIHRALYYDLISSPDH 120
QY 121 TYKELLDVTAPQKNLKSASRIVEFEKKLRKSSVAPLEKSYGTRPVLGTGNRLDLOEI 180
Db 121 TYKELLDVTAPQKNLKSASRIVEFEKKLRKSSVAPLEKSYGTRPVLGTGNRLDLOEI 180
QY 181 NNWVQAQMKGLARSTKEIPDEISILLGVHAHFGQWVTKFDSKTSLEDFYLDERTVR 240
Db 181 NNWVQAQMKGLARSTKEIPDEISILLGVHAHFGQWVTKFDSKTSLEDFYLDERTVR 240
QY 241 VPMMSDPKAVLRYGLSDLSCKIAQLPLTGSMSIIFPLPKVTQNTLIEESLTSFIHD 300
Db 241 VPMMSDPKAVLRYGLSDLSCKIAQLPLTGSMSIIFPLPKVTQNTLIEESLTSFIHD 300
QY 301 IDRELKTQVAVLTVPKLSYEGEVTKSLOEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
Db 301 IDRELKTQVAVLTVPKLSYEGEVTKSLOEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
QY 361 GFENWEDGAGTTPSPGLQPAHLTPPLDYHLNQPFIFVLRDTDTGALLFIGKILDPGRP 418
Db 361 GFENWEDGAGTTPSPGLQPAHLTPPLDYHLNQPFIFVLRDTDTGALLFIGKILDPGRP 418

RESULT 5
ABU10031
XX ID ABU10031 standard; protein; 418 AA.
XX AC ABU10031;
XX DT 06-AUG-2003 (first entry)
XX DE Human pigment epithelium-derived factor PEDF.
XX KW Human; pigment epithelium-derived growth factor; PEDF; cytostatic;
KW antiarteriosclerotic; antidiabetic; ophthalmological; antiarthritic;
KW gene therapy; Wilms' tumour; prostate cancer; cancer; neovascularisation;
KW haemangioma; atherosclerosis; diabetic retinopathy; arthritis;
KW pre-cancerous lesion; nasal polyp.
XX OS Homo sapiens.
XX PN US2003064917-A1.
XX PD 03-APR-2003.
XX PF 26-JUN-2002; 2002US-00180959.
XX PR 23-JUL-1998; 98US-00122079.
XX PR 23-JUL-1998; 98WO-US015228.
XX PR 23-FEB-2000; 2000US-00511683.
XX PR 23-JUN-2000; 2000US-00603478.
XX PA (CRAW/) CRAWFORD S E.
XX PA (DOLL/) DOLL J A.
XX PA (STEL/) STELLMACH V.
XX PI Crawford SE, Doll JA, Stellmach V;
XX WT; 2003-467440/44.
XX DR N-PSDB; ACA61620.
XX DX
XX PT Treating Wilms' tumor or prostate cancer in a mammal comprises providing
XX PT an exogenous PEDF to the mammal to treat the tumor or cancer.
XX PS Example 6; Fig 6A; 66pp; English.
XX CC The invention describes a method of treating Wilms' tumour or prostate
CC cancer in a mammal comprising providing an exogenous PEDF to the mammal
CC to treat the tumour or cancer. The method is useful in treating or
CC determining the severity of Wilms' tumour or prostate cancer in a mammal.
CC The method may also be used in preventing or treating other disorders
CC associated with neovascularisation, such as haemangioma, atherosclerosis,

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CC diabetic retinopathy, arthritis, and other pre-cancerous lesions like
CC nasal polyps. This is the amino acid sequence of human pigment epithelium
CC -drived factor (PEDF)
XX
XX Sequence 418 AA;
XX
Query Match 99.7%; Score 2125; DB 7; Length 418;
Best Local Similarity 99.5%; Pred. No. 3.3e-189;
Matches 416; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MCALVLLLCIGALLGHSSCONPPEEGSPDPDSTGALVEEEDPPFKVPVKNLAAAVSN 60
Db 1 MCALVLLLCIGALLGHSSCONPPEEGSPDPDSTGALVEEEDPPFKVPVKNLAAAVSN 60
QY 61 FGYDLVRSSMSPTTNVLLSPLSVATALSALSGADERTESIHRALYYDLISSPDH 120
Db 61 FGYDLVRSSMSPTTNVLLSPLSVATALSALSGADERTESIHRALYYDLISSPDH 120
QY 121 TYKELLDVTAPQKNLKSASRIVEFEKKLRKSSVAPLEKSYGTRPVLGTGNRLDLOEI 180
Db 121 TYKELLDVTAPQKNLKSASRIVEFEKKLRKSSVAPLEKSYGTRPVLGTGNRLDLOEI 180
QY 181 NNWVQAQMKGLARSTKEIPDEISILLGVHAHFGQWVTKFDSKTSLEDFYLDERTVR 240
Db 181 NNWVQAQMKGLARSTKEIPDEISILLGVHAHFGQWVTKFDSKTSLEDFYLDERTVR 240
QY 241 VPMMSDPKAVLRYGLSDLSCKIAQLPLTGSMSIIFPLPKVTQNTLIEESLTSFIHD 300
Db 241 VPMMSDPKAVLRYGLSDLSCKIAQLPLTGSMSIIFPLPKVTQNTLIEESLTSFIHD 300
QY 301 IDRELKTQVAVLTVPKLSYEGEVTKSLOEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
Db 301 IDRELKTQVAVLTVPKLSYEGEVTKSLOEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
QY 361 GFENWEDGAGTTPSPGLQPAHLTPPLDYHLNQPFIFVLRDTDTGALLFIGKILDPGRP 418
Db 361 GFENWEDGAGTTPSPGLQPAHLTPPLDYHLNQPFIFVLRDTDTGALLFIGKILDPGRP 418

RESULT 6
AAR44800
XX ID AAR44800 standard; protein; 418 AA.
XX AC AAR44800;
XX DT 25-MAR-2003 (revised)
XX DT 22-JUN-1994 (first entry)
XX DE Sequence of retinal pigmented epithelium-derived neurotrophic factor
XX DE (PEDNF).
XX KW Serine protease inhibitor gene family; neurotrophic activity;
XX KW tumour therapy.
XX OS Homo sapiens.
XX PN WO9324529-A1.
XX PD 09-DEC-1993.
XX PF 04-JUN-1993; 93WO-US005358.
XX PR 04-JUN-1992; 92US-00894215.
XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX PI Johnson IV, Tombran-Tink J;
XX WPI; 1993-405734/50.
XX DR N-PSDB; AAQ53160.
XX PT Purified retinal pigmented epithelium derived neurotrophic factor - is
XX used for treating tumours, ocular disease or nerve damage or as serine

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PT  protease inhibitors for treating e.g. ischaemia, etc.
XX  Claim 1; Page 44-46; 55pp; English.
XX  PEDNF was isolated from cultured retinal pigment epithelium (RPE) cells.
CC  Oligos were constructed from the sequence derived from PEDNF and used as
CC  primers in PCR amplification of a human fetal eye Charon BS cDNA library
CC  to obtain DNA encoding PEDNF. The oligo primers were constructed against
CC  the following peptides: PEDNF 13 - residues 236- 244 (AAQ53161); and
CC  PEDNF 2 - residues 107-135 (AAQ53162). PEDNF is a unique member of the
CC  serine protease inhibitor (SERPIN) gene family. (Updated on 25-MAR-2003
XX  to correct PN field.)
XX  Sequence 418 AA;
XX  Query Match      98.8%; Score 2106; DB 2; Length 418;
XX  Best Local Similarity 99.0%; Pred. No. 2e-187;
XX  Matches 414; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY  1 MQALVLLLCIGALLGHSSCONPASPPEGSPDPDSTGALVEEDPPFFKVPVVKLAASN 60
DB  1 MQALVLLLCIGALLGHSSWQNPASPPEGSPDPDSTGALVEEDPPFFKVPVVKLAASN 60
QY  61 FGVDLYRVSSMPTTNVLLSPLSVATALSALSGAQRTESIHRALYYDLISSPDH 120
DB  61 FGVDLYRVSSMPTTNVLLSPLSVATALSALSGAQRTESIHRALYYDLISSPDH 120
QY  121 TYKELDTVTAPQKNLKSASRIVFEKKLRKSFVAPLEKSYGTRPRVLTGNPRLDQEI 180
DB  121 TYKELDTVTAPQKNLKSASRIVFEKKLRKSFVAPLEKSYGTRPRVLTGNPRLDQEI 180
QY  181 NNWVQAMQKGLARSTKEIPDEISILLGVAFHKGQWTKFDSRKTSLEDFYLDERTVR 240
DB  181 NNWVQAMQKGLARSTKEIPDEISILLGVAFHKGQWTKFDSRKTSLEDFYLDERTVR 240
QY  241 VPWMSDPKAVLYRGDSDLSKIAQLPLTGSMSIIFPLPKVTQNLTLIESLTSFIHD 300
DB  241 VPWMSDPKAVLYRGDSDLSKIAQLPLTGSMSIIFPLPKVTQNLTLIESLTSFIHD 300
QY  301 IDRELKTVQAVLTVPKLKSVEGEVTKSLQEMKLSLFDSPFSKITGKIKTQVEHRA 360
DB  301 IDRELKTVQAVLTVPKLKSVEGEVTKSLQEMKLSLFDSPFSKITGKIKTQVEHRA 360
QY  361 GFENWEDAGTTPSGLOPAHLTFPLDYHLNQPFIFVLRDITDTGALLFIKILDPGRP 418
DB  361 GFENWEDAGTTPSGLOPAHLTFPLDYHLNQPFIFVLRDITDTGALLFIKILDPGRP 418
RESULT 7
ABR58379 standard; protein; 418 AA.
XX  ABR58379;
XX  07-JUL-2003 (first entry)
XX  Human NOV7a.
XX  Human; NOV; antidiabetic; anorectic; antibacterial; virucide;
KW  immunomodulator; cytostatic; nootropic; neuroprotective; dyslipidaemia;
KW  antiparkinsonian; antilipaeamic; gene therapy; metabolic disorder;
KW  diabetes; obesity; infection; cachexia; cancer; Parkinson's disease;
KW  neurodegenerative disorder; Alzheimer's disease; immune disorder;
KW  haematopoietic disorder.
XX  Homo sapiens.
XX  WO2003029423-A2.
XX  10-APR-2003.
XX  02-OCT-2002; 2002WO-US031358.
XX

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PR  02-OCT-2001; 2001US-0325483P.
PR  05-OCT-2001; 2001US-0327342P.
PR  09-OCT-2001; 2001US-0327917P.
PR  09-OCT-2001; 2001US-0328029P.
PR  09-OCT-2001; 2001US-0328044P.
PR  12-OCT-2001; 2001US-0328056P.
PR  12-OCT-2001; 2001US-0328849P.
PR  15-OCT-2001; 2001US-0329414P.
PR  17-OCT-2001; 2001US-0330142P.
PR  22-OCT-2001; 2001US-0341059P.
PR  24-OCT-2001; 2001US-0339266P.
PR  24-OCT-2001; 2001US-0343629P.
PR  29-OCT-2001; 2001US-0349575P.
PR  01-NOV-2001; 2001US-0346357P.
PR  12-APR-2002; 2002US-0371972P.
PR  12-APR-2002; 2002US-0371980P.
PR  17-APR-2002; 2002US-0373261P.
PR  19-APR-2002; 2002US-0373805P.
PR  23-APR-2002; 2002US-0374738P.
PR  16-MAY-2002; 2002US-0381101P.
PR  17-MAY-2002; 2002US-0381635P.
PR  29-MAY-2002; 2002US-0383830P.
PR  01-OCT-2002; 2002US-00262839.
XX  (CURA-) CURAGEN CORP.
XX  Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Catterton E;
XX  Edinger SR, Ellerman K, Gerlach VL, Gorman L, Guo X, Ji W;
XX  Kekuda R, Leach MD, Li L, Miller CE, Patturajan M, Rieger DK;
XX  Rothberg ME, Shinkens RA, Smithson G, Spytek KA, Taupier RJ;
XX  Vernet CAM, Voss EZ, Zerhusen BD, Zhong M;
XX  WPI; 2003-381625/36.
XX  N-PSDB; ACC72091.
XX  NOVX polypeptides and nucleic acids useful for diagnosing, preventing or
XX  treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or
XX  dyslipidemia, and in chromosome mapping, tissue typing or
XX  pharmacogenomics.
XX  Claim 1; Page 129; 487pp; English.
XX  The present invention relates to novel human NOV proteins and their
XX  coding sequences (ACC72075-ACC72181 and ABR58363-ABR58469). The NOV
XX  proteins are useful in manufacturing a medicament for treating a syndrome
XX  associated with a human disease. The NOV proteins and coding sequences
XX  may be used to diagnose, treat or prevent metabolic disorders such as
XX  diabetes or obesity, infections, cachexia, cancer, neurodegenerative
XX  disorders such as Alzheimer's disease or Parkinson's disease, immune
XX  disorders, haematopoietic disorders and various dyslipidaemias
XX  SQ  Sequence 418 AA;
XX  Query Match      98.8%; Score 2106; DB 6; Length 418;
XX  Best Local Similarity 99.0%; Pred. No. 2e-187;
XX  Matches 414; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY  1 MQALVLLLCIGALLGHSSCONPASPPEGSPDPDSTGALVEEDPPFFKVPVVKLAASN 60
DB  1 MQALVLLLCIGALLGHSSWQNPASPPEGSPDPDSTGALVEEDPPFFKVPVVKLAASN 60
QY  61 FGVDLYRVSSMPTTNVLLSPLSVATALSALSGAQRTESIHRALYYDLISSPDH 120
DB  61 FGVDLYRVSSMPTTNVLLSPLSVATALSALSGAQRTESIHRALYYDLISSPDH 120
QY  121 TYKELDTVTAPQKNLKSASRIVFEKKLRKSFVAPLEKSYGTRPRVLTGNPRLDQEI 180
DB  121 TYKELDTVTAPQKNLKSASRIVFEKKLRKSFVAPLEKSYGTRPRVLTGNPRLDQEI 180
QY  181 NNWVQAMQKGLARSTKEIPDEISILLGVAFHKGQWTKFDSRKTSLEDFYLDERTVR 240
DB  181 NNWVQAMQKGLARSTKEIPDEISILLGVAFHKGQWTKFDSRKTSLEDFYLDERTVR 240

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QY 241 VPMSPDKAVLYGLDLSCKIAQLPTGSMSTIFFPLKVTQCNLTLEESLTSBFHD 300
 Db 241 VPMSPDKAVLYGLDLSCKIAQLPTGSMSTIFFPLKVTQCNLTLEESLTSBFHD 300
 QY 301 IDRELKTVQAVLTVPKLSYEGEVTKSLQEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
 Db 301 IDRELKTVQAVLTVPKLSYEGEVTKSLQEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
 QY 361 GFEWNEGAGTTPSPGLOPAHLTPPLDYHLNQPPFVFLRDTDTGALLFIGKILDPGRP 418
 Db 361 GFEWNEGAGTTPSPGLOPAHLTPPLDYHLNQPPFVFLRDTDTGALLFIGKILDPGRP 418

RESULT 8
 ID ABG72122 standard; protein; 418 AA.
 XX
 AC ABG72122;
 DT 30-JAN-2003 (first entry)
 XX
 DE Human pigmented epithelium derived neurotrophic factor (PEDF).
 XX
 KW Human; retinal pigmented epithelium derived neurotrophic factor; PEDF;
 KW retinal disease; retinal tumour; retinoblastoma; retinal detachment;
 KW neuronal-retinal tumour; macular degeneration; retinitis pigmentosa;
 KW diabetic retinopathy; inherited and age-related pathology; tumour;
 KW ocular disease; nerve injury; serine protease related disorder;
 KW cystotic; ophthalmological; antiinflammatory; antidiabetic.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..18
 FT Protein /label= Signal_peptide
 FT # /label= Mature_PEDF
 XX
 US 6451763-B1.
 XX
 17-SEP-2002.
 XX
 29-AUG-1995; 95US-00520373.
 XX
 04-JUN-1992; 92US-00894215.
 PR 24-SEP-1992; 92US-00952796.
 PR 25-JUL-1994; 94US-00279979.
 PR 25-JAN-1995; 95US-00377710.
 XX
 (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Tombran-Tink J, Chader GU, Becerra SP, Rodriguez IR, Steele FR;
 PI Johnson LV;
 XX
 DR WPI; 2003-056723/05.
 DR N-PSDB; ABS57266.
 XX
 Treating retinal disease such as retinal tumors, retinitis pigmentosa,
 FT macular degeneration and diabetic retinopathy, in a subject, involves
 FT administering Pigment Epithelium Derived Factor to the subject.
 XX
 PS Claim 1; Col 61-64; 53pp; English.
 XX
 CC The present invention relates to the isolation of a human retinal
 CC pigmented epithelium derived neurotrophic factor (PEDF), and
 CC polynucleotide sequences encoding it. The gene encoding human PEDF maps
 CC to chromosome 17p13.1-pter. The invention also describes a truncated
 CC version of PEDF referred to as PEDF-BH, vectors comprising nucleic acids
 CC encoding PEDF or PEDF-BH, and a method of using these sequences to treat
 CC retinal diseases such as retinal tumors (e.g. retinoblastoma), neuronal-
 CC retinal tumors, macular degeneration, retinitis pigmentosa, retinal
 CC detachment, diabetic retinopathy, inherited and age-related pathologies,
 CC tumours, ocular diseases, nerve injuries, and conditions resulting from

CC the activity of serine proteases. The present sequence represents human
 CC PEDF
 SQ Sequence 418 AA;
 Query Match 98.4%; Score 2097; DB 6; Length 418;
 Best Local Similarity 98.8%; Pred. No. 1.3e-186;
 Matches 413; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MQALVLLLCIGALLGHSCQNPASPPPEGSPDDSTGALVEEDPPFFKVPVKNLAAAVSN 60
 Db 1 MQALVLLLCIGALLGHSCQNPASPPPEGSPDDSTGALVEEDPPFFKVPVKNLAAAVSN 60
 QY 61 FGVDLYRVRSSMPTTNVLLSPLSVATALSALSGAEQRTESIIRALYYDLTISSPDH 120
 Db 61 FGVDLYRVRSSMPTTNVLLSPLSVATALSALSGAEQRTESIIRALYYDLTISSPDH 120
 QY 121 TYKELLDTVTAPQKNLKSASRIVFEXKLRIRKSSVAPLEKSYGTRPRVLTGNPLDLQEI 180
 Db 121 TYKELLDTVTAPQKNLKSASRIVFEXKLRIRKSSVAPLEKSYGTRPRVLTGNPLDLQEI 180
 QY 181 NNWQAQMKGLABSTKEIPDEISILLGVAFHFGQVTKTDSRKTSLIEDFYLDEERTVR 240
 Db 181 NNWQAQMKGLABSTKEIPDEISILLGVAFHFGVTKFDSRKTSLIEDFYLDEERTVR 240
 QY 241 VPMSPDKAVLYGLDLSCKIAQLPTGSMSTIFFPLKVTQCNLTLEESLTSBFHD 300
 Db 241 VPMSPDKAVLYGLDLSCKIAQLPTGSMSTIFFPLKVTQCNLTLEESLTSBFHD 300
 QY 301 IDRELKTVQAVLTVPKLSYEGEVTKSLQEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
 Db 301 IDRELKTVQAVLTVPKLSYEGEVTKSLQEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
 QY 361 GFEWNEGAGTTPSPGLOPAHLTPPLDYHLNQPPFVFLRDTDTGALLFIGKILDPGRP 418
 Db 361 GFEWNEGAGTTPSPGLOPAHLTPPLDYHLNQPPFVFLRDTDTGALLFIGKILDPGRP 418

RESULT 9
 ADB9089
 ID ADB9089 standard; protein; 418 AA.
 XX
 AC ADB9089;
 DT 04-DEC-2003 (first entry)
 DE Human retinal pigment epithelial-derived factor (PEDF).
 XX
 KW Human; retinal pigment epithelial-derived neurotrophic factor; PEDF;
 KW tumour; ocular disease; neuronal cell pathology; serine protease;
 KW blood coagulation; thrombosis; bacterial infection; parasitic infection;
 KW elastosis; vascular disorder; fibrinoid formation; coagulation disorder;
 KW arteriosclerosis; ischaemia; arthrosis diabetes; emphysema; arthritis;
 KW septic shock; lung disease; complement activation; ulcer;
 KW ulcerative colitis; pancreatitis; psoriasis; fibrinolytic disease;
 KW arthropathy; bone resorption; hypertension; congestive heart failure;
 KW cirrhosis; protease allergy; chromosome 17p13.1-pter.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..18
 FT Protein /note= "Signal peptide"
 FT /note= "Mature PEDF"
 XX
 US 2003096750-A1.
 XX 22-MAY-2003.
 PF 09-AUG-2002; 2002US-00216373.
 XX 04-JUN-1992; 92US-00894215.

PR 24-SEP-1992; 92US-00952796.
PE 29-AUG-1995; 95US-00520373.
XX (TOMB/) TOMBRAN-TINK J.
FA (STEE/) STEELE F R.
FA (CHAD/) CHADER G J.
FA (BEC/) BECERRA S P.
PA (JOHN/) JOHNSON L V.
PA (RODR/) RODRIGUEZ I R.
XX
PI Tombran-Tink J, Steele FR, Chader GJ, Becerra SP, Johnson LV;
FI Rodriguez IR;
XX
DR WPI; 2003-743982/70.
DR N-PSDB; ADB99088.
XX
XX New purified retinal pigmented epithelium derived neurotrophic factor
PT composition, useful for treating tumors, i.e. retinal tumor, ocular
PT disease, neuronal cell pathologies, coagulation disorders or
PT arteriosclerosis.
XX
XX Claim 3; SEQ ID NO 2; 58pp; English.
XX
XX The invention relates to a composition comprising purified retinal
CC pigmented epithelium derived neurotrophic factor (PEDF). The PEDF
CC proteins comprise ADB99089, ADB99090 or sequences equivalent to but not
CC identical to ADB99089. Human PEDF is encoded by ADB99088. Also included
CC are purifying PEDF, producing PEDF comprising expressing the DNA sequence
CC encoding the PEDF in a host cell, a recombinant DNA molecule comprising a
CC genomic DNA fragment for PEDF (appearing as ADB99091 - ADB99093), a
CC vector comprising a PEDF nucleic acid molecule, an organism transformed
CC with a recombinant DNA molecule comprising a retinal PEDF cDNA, a host
CC cell containing the vector, a recombinantly produced PEDF protein which
CC is free from the risks normally associated with proteins isolated or
CC purified from a naturally occurring source organism and a purified human
CC genomic DNA molecule encoding a PEDF protein. The purified retinal
CC pigmented epithelium derived neurotrophic factor is useful for treating
CC tumors, i.e. retinal tumor, ocular disease, neuronal cell pathologies,
CC or conditions resulting from the activity of serine proteases, e.g.
CC excessive or unwanted blood coagulation, thrombosis, bacterial infection,
CC parasitic infection, elastosis, vascular disorders involving fibrinoid
CC formation, coagulation disorders, arteriosclerosis, ischaemia, arthroses
CC diabetes, emphysema, arthritis, septic shock, lung diseases, excessive
CC complement activation, ulcers, ulcerative colitis, pancreatitis,
CC psoriasis, fibrinolytic diseases, arthropathy, bone resorption,
CC hypertension, congestive heart failure, cirrhosis, or allergy caused by
CC proteases. The present sequence represents human retinal pigmented
CC epithelium derived neurotrophic factor (PEDF).
XX
SQ Sequence 418 AA;

Query Match 98.4%; Score 2097; DB 7; Length 418;
Best Local Similarity 98.8%; Pred.No. 1.3e-186;
Matches 413; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MQALVLLICIGALGHSCQNPASPPREGSDPDSTGALVEEDPPFPKVPVKLAASVN 60
DB 1 MQALVLLICIGALGHSCQNPASPPREGSDPDSTGALVEEDPPFPKVPVKLAASVN 60
QY 61 FGVDLYRVRSMSPPTNVLLSPLSVATALSALSILGAEQRTESIHRALYDLISSPDHG 120
DB 61 FGVDLYRVRSMSPPTNVLLSPLSVATALSALSILGAEQRTESIHRALYDLISSPDHG 120
QY 121 TYKELDDVTAPQKNLSASRIVEKKLRIRKSSVAPLEKSYGTRPRVLGNPFLDLOEI 180
DB 121 TYKELDDVTAPQKNLSASRIVEKKLRIRKSSVAPLEKSYGTRPRVLGNPFLDLOEI 180
QY 181 NNWVQAQMGKGLARSTKEIPDEISILLGVAFHGQWVTKFSDSKTSLEDFYLDERTVR 240
DB 181 NNWVQAQMGKGLARSTKEIPDEISILLGVAFHGQWVTKFSDSKTSLEDFYLDERTVR 240
QY 241 VPMMSDPKAVLYRGDLSLCKIAQLPLTGRMSIIFFLPKLVTONLTLIEESLTSEFIHD 300

DB 241 VPMMSDPKAVLYRGDLSLCKIAQLPLTGRMSIIFFLPKLVTONLTLIEESLTSEFIHD 300
QY 301 IDRELKTVQAVLTVPKILSVGEVTKSLOENKLOSLEDSDFSKITGKPIKLTQVHRA 360
DB 301 IDRELKTVQAVLTVPKILSVGEVTKSLOENKLOSLEDSDFSKITGKPIKLTQVHRA 360
QY 361 GFENWEDGAGTTTSPGLOPAHLTFPDLVHNLNPFIFVLRTDTGALLFTGKILDRPG 418
DB 361 GFENWEDGAGTTTSPGLOPAHLTFPDLVHNLNPFIFVLRTDTGALLFTGKILDRPG 418
RESULT 10
AAR90288
ID AAR90288 standard; protein; 379 AA.
XX
AC AAR90288;
XX
DT 16-JAN-1997 (first entry)
XX
DE Modified pigment epithelium-derived factor (rPEDF).
XX
XX Pigment epithelium-derived factor; PEDF; neuronal cells; neurons;
KW glial cells; gliastatic; gliosis; central nervous system; CNS;
KW neurodegenerative disease; injury; neurotrophic; brain cells;
KW Parkinson's disease; photoreceptor cells; retina; inhibition;
KW proliferation; immunoassay; antibody; ageing; degenerative disease.
XX
OS Homo sapiens.
XX
PN W09533480-A1.
XX
PD 14-DEC-1995.
XX
PF 06-JUN-1995; 95WO-US007201.
XX
PR 07-JUN-1994; 94US-00257963.
XX
PR 30-DEC-1994; 94US-00367841.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Chader GJ, Becerra SP, Schwartz JP, Taniwaki T;
XX WPI; 1996-039966/04.
XX
XX Use of pigment epithelium derived factor - for enhancing neuronal cell
PT survival and inhibiting glial cell proliferation, useful, e.g. in CNS
PT cell culture or to treat neuro-degenerative diseases.
XX
XX Disclosure; Page 66-67; 151pp; English.
XX
XX Pigment epithelium-derived factor (PEDF) has both neurotrophic and
CC gliastatic activity, making it useful in cases where neurons die quickly
CC and glia tend to proliferate (gliosis), e.g. in CNS cell culture, in
CC neurodegenerative diseases and in CNS injury. The neurotrophic effect
CC of PEDF is especially useful for enhancing survival of neuronal cell
CC cultures intended for use in transplantation. These include cultures of
CC human foetal brain cells and neural retina and photoreceptor cells. The
CC gliastatic activity of PEDF can be applied to inhibiting glial cell
CC proliferation in certain tumors. Antibodies directed against PEDF can be
CC used for inhibiting PEDF activity or in an immunoassay for determining
CC levels of PEDF in fluid, cellular or tissue samples e.g. for determining
CC ageing and/or other degenerative diseases. This sequence is designated
CC rPEDF and comprises the amino acid sequence Met-Asn-Arg-Ile fused to
CC Asp44-Pro418 of PEDF
XX
XX Sequence 379 AA;

Query Match 89.3%; Score 1904; DB 2; Length 379;
Best Local Similarity 99.7%; Pred.No. 1.2e-168;
Matches 374; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 44 DPFKVPVKLAASVNFQYDLYRVRSMSPPTNVLLSPLSVATALSALSILGAEQRTESI 103

Db 5 DFFKVPVKNKLAASVNFYDLYRVRSSMGPTTNVLLSPISVATLSALSGAEQRTESI 64
 QY 104 IHRALYDYLISSPDIHGTYKELLDTVTAPQNLKASRIVFEEKLRKSSFVAPLEKSYG 163
 Db 65 IHRALYDYLISSPDIHGTYKELLDTVTAPQNLKASRIVFEEKLRKSSFVAPLEKSYG 124
 QY 164 TRPVLTGNPRDLQEIINNWNVQAQMGKGLARSTKEIPDEISILLGLVAHFKGQWVTKFDS 223
 Db 125 TRPVLTGNPRDLQEIINNWNVQAQMGKGLARSTKEIPDEISILLGLVAHFKGQWVTKFDS 184
 QY 224 RKTSLDFYLDERTVRVPMMSDPKAVLRVGLSDLSCKIAQLPLTGSMIIIFFLPKVY 283
 Db 185 RKTSLDFYLDERTVRVPMMSDPKAVLRVGLSDLSCKIAQLPLTGSMIIIFFLPKVY 244
 QY 284 QNLTLIEESLTSEFIHDIIDRELKTVQAVLTVPKLSYEGETVTKSLQEMKLSLDFSPDF 343
 Db 245 QNLTLIEESLTSEFIHDIIDRELKTVQAVLTVPKLSYEGETVTKSLQEMKLSLDFSPDF 304
 QY 344 SKITGKPIKLTQVEHRAAGFEWNEAGAGTTPSPGLQPAHLTFPLDYHLNQPFIFVLRTDT 403
 Db 305 SKITGKPIKLTQVEHRAAGFEWNEAGAGTTPSPGLQPAHLTFPLDYHLNQPFIFVLRTDT 364
 QY 404 GALLFIGKILDPRGP 418
 Db 365 GALLFIGKILDPRGP 379

RESULT 11
 ABG72123
 ID ABG72123 standard; protein; 379 AA.
 AC ABG72123;
 DT 30-JAN-2003 (first entry)
 XX Truncated version of human PEDF, PEDF-BH.
 KW Human; retinal pigmented epithelium derived neurotrophic factor; PEDF;
 KW retinal disease; retinal tumour; retinoblastoma; retinal detachment;
 KW neuronal retinal tumour; macular degeneration; retinitis pigmentosa;
 KW diabetic retinopathy; inherited and age-related pathology; tumour;
 KW ocular disease; nerve injury; serine protease related disorder;
 KW cytoskeletal; ophthalmological; antiinflammatory; antidiabetic; mutant;
 KW mitein; PEDF-BH.
 OS Homo sapiens.
 OS Synthetic.

Key Location/Qualifiers
 FT Peptide 1..4
 FT /note= "N-terminal fusion peptide"
 FT Region 5..379
 FT /note= "Corresponds to amino acid residues 44-418 of
 human PEDF (ABG72122)"

US6451763-B1.
 17-SEP-2002.
 29-AUG-1995; 95US-00520373.
 04-JUN-1992; 92US-00894215.
 24-SEP-1992; 92US-00952796.
 25-JUL-1994; 94US-00279979.
 25-JAN-1995; 95US-00377710.
 (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Tombran-Tink J, Chader GJ, Becerra SP, Rodriguez IR, Steele PR;
 PI Johnson LV;
 DR WPI; 2003-056723/05.

PT Treating retinal disease such as retinal tumors, retinitis pigmentosa,
 PT macular degeneration and diabetic retinopathy, in a subject, involves
 XX administering Pigment Epithelium Derived Factor to the subject.
 PS Claim 1; Col 65; 53pp; English.
 XX The present invention relates to the isolation of a human retinal
 CC pigmented epithelium derived neurotrophic factor (PEDF), and
 CC polynucleotide sequences encoding it. The gene encoding human PEDF maps
 CC to chromosome 17p13.1-pter. The invention also describes a truncated
 CC version of PEDF referred to as PEDF-BH, vectors comprising nucleic acids
 CC encoding PEDF or PEDF-BH, and a method of using these sequences to treat
 CC retinal diseases such as retinal tumors (e.g. retinoblastoma), neuronal-
 CC retinal tumors, macular degeneration, retinitis pigmentosa, retinal
 CC detachment, diabetic retinopathy, inherited and age-related pathologies,
 CC tumours, ocular diseases, nerve injuries, and conditions resulting from
 CC the activity of serine proteases. The present sequence represents human
 CC PEDF-BH which has an N-terminal fusion to Asp44-Pro418 of human PEDF
 CC (ABG72122), such that Met1-Glu43 of human PEDF are deleted in this
 CC version
 XX Sequence 379 AA;
 SQ

Query Match 87.8%; Score 1870; DB 6; Length 379;
 Best Local Similarity 98.7%; Pred. No. 1.8e-165;
 Matches 370; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 44 DFFKVPVKNKLAASVNFYDLYRVRSSMGPTTNVLLSPISVATLSALSGAEQRTESI 103
 Db 5 DFFKVPVKNKLAASVNFYDLYRVRSSMGPTTNVLLSPISVATLSALSGAEQRTESI 64
 QY 104 IHRALYDYLISSPDIHGTYKELLDTVTAPQNLKASRIVFEEKLRKSSFVAPLEKSYG 163
 Db 65 IHRALYDYLISSPDIHGTYKELLDTVTAPQNLKASRIVFEEKLRKSSFVAPLEKSYG 124
 QY 164 TRPVLTGNPRDLQEIINNWNVQAQMGKGLARSTKEIPDEISILLGLVAHFKGQWVTKFDS 223
 Db 125 TRPVLTGNPRDLQEIINNWNVQAQMGKGLARSTKEIPDEISILLGLVAHFKGQWVTKFDS 184
 QY 224 RKTSLDFYLDERTVRVPMMSDPKAVLRVGLSDLSCKIAQLPLTGSMIIIFFLPKVY 283
 Db 185 RKTSLDFYLDERTVRVPMMSDPKAVLRVGLSDLSCKIAQLPLTGSMIIIFFLPKVY 244
 QY 284 QNLTLIEESLTSEFIHDIIDRELKTVQAVLTVPKLSYEGETVTKSLQEMKLSLDFSPDF 343
 Db 245 QNLTLIEESLTSEFIHDIIDRELKTVQAVLTVPKLSYEGETVTKSLQEMKLSLDFSPDF 304
 QY 344 SKITGKPIKLTQVEHRAAGFEWNEAGAGTTPSPGLQPAHLTFPLDYHLNQPFIFVLRTDT 403
 Db 305 SKITGKPIKLTQVEHRAAGFEWNEAGAGTTPSPGLQPAHLTFPLDYHLNQPFIFVLRTDT 364
 QY 404 GALLFIGKILDPRGP 418
 Db 365 GALLFIGKILDPRGP 379

RESULT 12
 ADB99090
 ID ADB99090 standard; protein; 379 AA.
 XX ADB99090;
 AC ADB99090;
 XX 04-DEC-2003 (first entry)
 DT Human retinal pigment epithelial-derived factor, PEDF-BH.
 DE Human; retinal pigment epithelial-derived neurotrophic factor; PEDF-BH;
 KW tumour; ocular disease; neuronal cell pathology; serine protease;
 KW blood coagulation; thrombosis; bacterial infection; parasitic infection;
 KW elastosis; vascular disorder; fibroid formation; coagulation disorder;
 KW arteriosclerosis; ischaemia; arthrosis diabetes; emphysema; arthritis;
 KW septic shock; lung disease; complement activation; ulcer;
 KW ulcerative colitis; pancreatitis; psoriasis; fibrinolytic disease;

KW	arthropathy; bone resorption; hypertension; congestive heart failure;	
KW	cirrhosis; protease allergy; chromosome 17p13.1-pter.	
XX	Synthetic.	
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Misc-difference 1.4	/note= "Replaces amino acids 1-43 of the wild-type PEDF protein"
FT		
XX		
XX	US2003096750-A1.	
XX		
PD	22-MAY-2003.	
XX		
XX	09-AUG-2002; 2002US-00216373.	
XX		
PR	04-JUN-1992; 92US-00894215.	
PR	24-SEP-1992; 92US-00352796.	
PR	29-AUG-1995; 95US-00520373.	
XX		
XX	(TOMB/) TOMBRAN-TINK J.	
PA	(STEE/) STEELE F R.	
PA	(CHAD/) CHADER G J.	
PA	(BECE/) BECERRA S P.	
PA	(JOHN/) JOHNSON L V.	
PA	(RODR/) RODRIGUEZ I R.	
XX		
PI	Tombran-Tink J, Steele FR, Chader GJ, Becerra SP, Johnson LV, Rodriguez IR;	
PI		
XX	WPI; 2003-743982/70.	
DR		
XX		
FT	New purified retinal pigmented epithelium derived neurotrophic factor	
FT	composition, useful for treating tumors, i.e. retinal tumor, ocular	
PT	disease, neuronal cell pathologies, coagulation disorders or	
PT	arteriosclerosis.	
XX		
XX	Claim 5; SEQ ID NO 3; 58pp; English.	
PS		
XX		
CC	The invention relates to a composition comprising purified retinal	
CC	pigmented epithelium derived neurotrophic factor (PEDF). The PEDF	
CC	proteins comprise ADB99089, ADB99090 or sequences equivalent to but not	
CC	identical to ADB99089. Human PEDF is encoded by ADB99088. Also included	
CC	are purifying PEDF, producing PEDF comprising expressing the DNA sequence	
CC	encoding the PEDF in a host cell, a recombinant DNA molecule comprising a	
CC	genomic DNA fragment for PEDF (appearing as ADB99091 - ADB99093), a	
CC	vector comprising a PEDF nucleic acid molecule, an organism transformed	
CC	with a recombinant DNA molecule comprising a retinal PEDF cDNA, a host	
CC	cell containing the vector, a recombinantly produced PEDF protein which	
CC	is free from the risks normally associated with proteins isolated or	
CC	purified from a naturally occurring source organism and a purified human	
CC	genomic DNA molecule encoding a PEDF protein. The purified retinal	
CC	pigmented epithelium derived neurotrophic factor is useful for treating	
CC	tumors, i.e. retinal tumor, ocular disease, neuronal cell pathologies,	
CC	or conditions resulting from the activity of serine proteases, e.g.	
CC	excessive or unwanted blood coagulation, thrombosis, bacterial infection,	
CC	parasitic infection, elastosis, vascular disorders involving fibrinoid	
CC	formation, coagulation disorders, arteriosclerosis, ischaemia, arthroses	
CC	diabetes, emphysema, arthritis, septic shock, lung diseases, excessive	
CC	complement activation, ulcers, ulcerative colitis, pancreatitis,	
CC	porriasis, fibrinolytic disease, arthropathy, bone resorption,	
CC	hypertension, congestive heart failure, cirrhosis, or allergy caused by	
CC	proteases. The present sequence represents a human retinal pigmented	
CC	epithelium derived neurotrophic factor PEDF-BH where amino acids 1-43 of	
CC	wild-type PEDF has been replaced by Met-Asn-Arg-Ile-Asp.	
XX		
SQ	Sequence 379 AA;	
	Query Match	
	Best Local Similarity 87.8%; Score 1870; DB 7; Length 379;	
	Matches 370; Conservative 98.7%; Pred. No. 1.8e-165;	
	Indels 0; Gaps 0;	

QY	44	DPFFKVPVNVKLAASVNSFGYDLYRVRSSMPTTNVLLSPLSVATLSALSGAEQRTESI	103
Db	5	DPFFKVPVNVKLAASVNSFGKOLYRVRSSMPTTNVLLSPLSVATLSALSGAEQRTESI	64
QY	104	IHRALYYDLISSPDHGTGKELLDVTAPQKVKASRIVFEKKLRKSSFVAPLEKSYG	163
Db	65	IHRALYYDLISSPDHGTGKELLDVTAPQKVKASRIVFEKKLRKSSFVAPLEKSYG	124
QY	164	TRPRVLTGNPRDLQEIINNVAQMKGLARSTKIPDEISILLGLVAHFKGQWTKFDS	223
Db	125	TRPRVLTGNPRDLQEIINNVAQMKGLARSTKIPDEISILLGLVAHFKGQWTKFDS	184
QY	224	RKTSLEDFYLDERTVRVPMVSDPKAVRLRYGLDLSCKIAQLPTGMSIIFFLPKVT	283
Db	185	RKTSLEDFYLDERTVRVPMVSDPKAVRLRYGLDLSCKIAQLPTGMSIIFFLPKVT	244
QY	284	QNLTIIEESLTSEFTHDRELKTVQAVLTVPKLSYEGETVKLSIQENKLSLQSLFSDPF	343
Db	245	QNLTIIEESLTSEFTHDRELKTVQAVLTVPKLSYEGETVKLSIQENKLSLQSLFSDPF	304
QY	344	SKITCKPIKLTQVEHRRAGFEMNEDGAGTTPSGQLQPAHLTFPLDYHLNQPFIFVLRTDT	403
Db	305	SKITCKPIKLTQVEHRRAGFEMNEDGAGTTPSGQLQPAHLTFPLDYHLNQPFIFVLRTDT	364
QY	404	GALLFIGKILDRGP 418	
Db	365	GALLFIGKILDRGP 379	
	RESULT 13		
	ABB57391		
ID	ABB57391	standard; protein; 418 AA.	
XX	AC	ABB57391;	
DT	07-AUG-2003	(revised)	
DT	08-MAR-2002	(first entry)	
XX	DE	Rat mucocardial cell proliferation associated polypeptide SEQ ID NO 36.	
XX	KW	Rat; heart; cardiant; myocardial necrosis; cardiac hypertrophy;	
XX	KW	cardiac insufficiency.	
OS	Rattus norvegicus.		
PN	WO200183705-A1.		
PD	08-NOV-2001.		
PF	27-APR-2001; 2001WO-JP003700.		
PR	27-APR-2000; 2000JP-00126741.		
XX	(KYOW) KYOWA HAKKO KOGYO KK.		
XX	Yamada Y, Sekine S, Kikuchi Y, Sakurada K;		
XX	WPI; 2002-075160/10.		
DR	N-PSDB; ABI99933.		
XX	Genes having differential expression in fetal and adult heart tissue		
PT	useful for screening potential drugs for promoting repair of damage		
PT	caused by myocardial necrosis.		
XX	Claim 53; Page 153-155; 171pp; Japanese.		
PS			
XX	The invention relates to gene sequences (ABI99915-ABI99934) having		
CC	modified expression in fetal heart tissue as compared to adult heart		
CC	tissue and the encoded proteins (ABB57375-ABB57392). The genes have		
CC	cardiant activity and may be useful in the promotion of the repair of		
CC	damage to heart tissue caused by myocardial necrosis. The gene sequences		
CC	are useful for screening potential compounds for the ability to influence		
CC	disease associated with myocardial necrosis. Drugs identified by the		

CC screening methods may be used to treat and prevent disease with which
 CC myocardial necrosis is associated, such as cardiac hypertrophy and
 CC cardiac insufficiency. Diagnosis of diseases such as those above is also
 CC disclosed. (Updated on 07-AUG-2003 to correct OS field.)

XX Sequence 418 AA;

Query Match 84.0%; Score 1789; DB 5; Length 418;
 Best Local Similarity 83.5%; Pred. No. 7.5e-158;
 Matches 348; Conservative 36; Mismatches 29; Indels 4; Gaps 3;

Qy 1 MQALVLLICIGALLGHSSCON-PASPEEGSPDSTG-ALVEEEDPFKVPVKNKLAAY 58
 Db 1 MQTLVLLWTGALLGHSSQNVDS--SQDSPADPTGEPVEEDDPFKAPVKNKLAAY 58
 Qy 59 SNFGYDLYRVRSSMPTTNVLLSPLSVATLSALSGAEQRTESIHRALYYDLISSPDI 118
 Db 59 SNFGYDLYRVRSSMPTTNVLLSPLSVATLSALSGAEQRTESIHRALYYDLINPDI 118
 Qy 119 HGTYKELLDTVTAPOKVLKASRIKSSVAPLEKSYGTRPRVLTCGNPRDLQ 178
 Db 119 HSTYKELLASVTAPEKNFKASRIKSSVAPLEKSYGTRPRILTCGNPRDLQ 178
 Qy 179 EINNWOQMKGLARSTKIPBISILLGVAFHFGQWTKFDSKTSLEDFYLDERT 238
 Db 179 EINNWOQMKGLARSTREMPALSILLGVAFHFGQWTKFDSKTSLEDFYLDERT 238
 Qy 239 VRVPMDSKAVLYRGLDSDLSCKIAQLPLTGSMSIFFLPLKVQNLILIEESLTSEFI 298
 Db 239 VRVPMDSKAVLYRGLDSDLSCKIAQLPLTGSMSIFFLPLKVQNLILIEESLTSEFI 298
 Qy 299 HDIDREKTVQAVLTVPKLSYEGEVTKLSQEMKQSLPDSDFSKITGKPKLTQVEH 358
 Db 299 HDIDREKTVQAVLTVPKLSYEGEVTKLSQEMKQSLPDSDFSKITGKPKLTQVEH 358
 Qy 359 RAGFEMNEDGAGTTPSGLOPAHLTPFLDYHLNQPFIFVLRDQDTGALLFIGKILDP 415
 Db 359 RAAEFMNEGAGTSSNDLPQVRLTPFLDYHLNRPFIIFVLRDQDTGALLFIGKILDP 415

RESULT 14

ID AAW97364 standard; peptide; 362 AA.

XX AAW97364;

XX 12-MAY-1999 (first entry)

DE Amino acid sequence of SLED (an antiangiogenic protein).

XX SLED; antiangiogenic protein; angiogenesis; endothelial cell migration;
 KW hair growth; tumour growth; angiogenic disease; reproduction;
 KW tumour prognosis; angiogenesis-related disorder.

XX Unidentified.

XX WO9904806-A1.

XX 04-FEB-1999.

XX 23-JUL-1998; 98WO-US015228.

XX 23-JUL-1997; 97US-00899304.

XX (NOUN) UNIV NORTHWESTERN.

XX Bouck NP, Dawson DW, Gillis PR;

XX WPI; 1999-142603/12.

XX Inhibiting endothelial cell migration and angiogenesis within a tissue -
 FT by providing exogenous SLED, useful to treat angiogenic diseases, and
 FT assess tumour severity.

XX Disclosure; Page 25-26; 28pp; English.

XX The present sequence represents SLED, an antiangiogenic protein.
 CC Angiogenesis within a tissue can be inhibited by providing exogenous SLED
 CC to endothelial cells associated with the tissue. Exogenous SLED can also
 CC be used to inhibit endothelial cell migration, stimulate hair growth, to
 CC inhibit tumour growth. It can also be used for determining the severity
 CC of a tumour, wherein absence of SLED indicates an early state of the
 CC advanced state, and presence of SLED indicates an early state of the
 CC tumour. The invention is used in the treatment of angiogenic diseases, to
 CC interfere with angiogenesis associated with reproductive functions, to
 CC assess the prognosis of tumours and other angiogenesis-related disorders,
 CC and to investigate angiogenesis in vitro

XX Sequence 362 AA;

Query Match 83.7%; Score 1784; DB 2; Length 362;

Best Local Similarity 100.0%; Pred. No. 1.8e-157;
 Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQALVLLICIGALLGHSSCONPASPEEGSPDSTGALVEEEDPFKVPVKNKLAAYVN 60

Db 1 MQALVLLICIGALLGHSSCONPASPEEGSPDSTGALVEEEDPFKVPVKNKLAAYVN 60

Qy 61 FGVDLYRVRSSMPTTNVLLSPLSVATLSALSGAEQRTESIHRALYYDLISSPDIHG 120

Db 61 FGVDLYRVRSSMPTTNVLLSPLSVATLSALSGAEQRTESIHRALYYDLISSPDIHG 120

Qy 121 TYKELLDTVTAPOKVLKASRIKSSVAPLEKSYGTRPRVLTCGNPRDLQEI 180

Db 121 TYKELLDTVTAPOKVLKASRIKSSVAPLEKSYGTRPRVLTCGNPRDLQEI 180

Qy 191 NNWVQAKMKGLARSTKIPBISILLGVAFHFGQWTKFDSKTSLEDFYLDERTVR 240

Db 191 NNWVQAKMKGLARSTKIPBISILLGVAFHFGQWTKFDSKTSLEDFYLDERTVR 240

Qy 241 VPMMSDKAVLYRGLDSDLSCKIAQLPLTGSMSIFFLPLKVQNLILIEESLTSEFIHD 300

Db 241 VPMMSDKAVLYRGLDSDLSCKIAQLPLTGSMSIFFLPLKVQNLILIEESLTSEFIHD 300

Qy 301 IDRELKTVQAVLTVPKLSYEGEVTKLSQEMKQSLPDSDFSKITGKPKLTQ 355

Db 301 IDRELKTVQAVLTVPKLSYEGEVTKLSQEMKQSLPDSDFSKITGKPKLTQ 355

RESULT 15

ID AAW08652 standard; protein; 362 AA.

XX AAW08652;

XX 18-DEC-2001 (first entry)

DE Human antiangiogenic protein SLED.

XX Human; SLED; antiangiogenic; antiinflammatory; antiarteriosclerotic;
 KW dermatological; antidiabetic; antipsoriatic; antiarthritic; vasotropic;
 KW ophthalmological; gynecological; cytostatic; tumour; psoriasis;
 KW scleroderma; neovascularisation; bacterial ulceration; muscle disease;
 KW intestinal adhesion; Crohn's disease; atherosclerosis; scleroderma;
 KW hypertrophic scar; eye injury; hypoxia; infection; diabetes;
 KW retinoblastoma; birth control.

OS Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..20

XX Protein 21..362

XX Region 44..157

XX /label= Signal_peptide

XX /label= Mature_SLED

XX /label= Active_fragment

FT Region /note= "Region displaying SLED activity"
FT 45..121
FT /label= Active fragment
XX /note= "Region displaying SLED activity"

FN US6288024-B1.

PD 11-SEP-2001.

XX 23-JUL-1998; 98US-00122079.

XX 23-JUL-1997; 97US-00899304.

XX (NOUN) UNIV NORTHWESTERN.

XX Bouck NP, Dawson DW, Gillis PR;

XX WPI; 2001-579337/65.

DR
XX
XX
PT Inhibition of angiogenesis/endothelial cell migration within a tissue
PT involves providing exogenous antiangiogenic protein to endothelial cells
PT associated with the tissue.

XX Disclosure; Col 12-14; 17pp; English.

XX
XX The invention relates to inhibition of angiogenesis/endothelial cell
XX migration within a tissue involving providing exogenous antiangiogenic
XX protein (SLED) to endothelial cells associated with the tissue. The
XX method is used for treating a host of diseases associated with
XX angiogenesis and for interfering with angiogenesis associated with
XX reproductive functions, for assessing the prognosis of tumours, useful
XX reagents for investigation of angiogenesis, for treating diseases and
XX disorders such as psoriasis, scleroderma, tumours of the skin,
XX neovascularisation as a consequence of infection like cat scratch
XX disease, bacterial ulceration or other skin disorders, blood vessels,
XX muscle diseases, joints, for treating disorders associated with
XX stimulation of endothelial cell migration such as intestinal adhesion,
XX Crohn's disease, atherosclerosis, scleroderma and hypertrophic scars, for
XX treating eye injury, hypoxia, infection, surgery, laser surgery,
XX diabetes, retinoblastoma or other diseases or disorders of the eye, to
XX modulate or prevent the occurrence of normal physiological conditions
XX associated with neovascularisation, can be used as a birth control,
XX attenuated neovascularisation associated with ovulation, implantation of
XX an embryo and placenta formation. The present sequence is human SLED

XX Sequence 362 AA;

Query Match 83.7%; Score 1784; DB 4; Length 362;
Best Local Similarity 100.0%; Pred. No. 1.8e-157;
Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQALVLLLCIGALGHSSCONPASPPEGSPDPDSTGALVEEDPFFKVPVNKLAASN 60
Db 1 MQALVLLLCIGALGHSSCONPASPPEGSPDPDSTGALVEEDPFFKVPVNKLAASN 60
Qy 61 FGVDLYVRSMPTTNVLLSPISVATLSALSLGAEQRTESIIRALYYDLISSPDH 120
Db 61 FGVDLYVRSMPTTNVLLSPISVATLSALSLGAEQRTESIIRALYYDLISSPDH 120
Qy 121 TYKELDTVTAPQKNLKSARIVFEKLRKSSFVAPLEKSYGTRPRVLTGNPRDLQEI 180
Db 121 TYKELDTVTAPQKNLKSARIVFEKLRKSSFVAPLEKSYGTRPRVLTGNPRDLQEI 180
Qy 181 NNWVQAOMKGLARSTKEIPDEISILLGVANFKGQWTKFDSRKTSLEDFYLDERTVR 240
Db 181 NNWVQAOMKGLARSTKEIPDEISILLGVANFKGQWTKFDSRKTSLEDFYLDERTVR 240
Qy 241 VPWMSDPKAVLRGLDSDLCKIAQLPLTGSMSIIFPLKVTQNLTLIEESLTSEFIHD 300
Db 241 VPWMSDPKAVLRGLDSDLCKIAQLPLTGSMSIIFPLKVTQNLTLIEESLTSEFIHD 300
Qy 301 IDRELKTVQAVLTVPKLSYGEVTKSLQEMKLSLFDSPDFSKITGPKILQTQ 355

Db 301 IDRELKTVQAVLTVPKLSYGEVTKSLQEMKLSLFDSPDFSKITGPKILQTQ 355

Search completed: September 1, 2004, 11:14:59
Job time : 131 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2004, 11:15:04 ; Search time 51 Seconds
(without alignments)

2578.592 Million cell updates/sec

Title: US-10-619-149-1

Perfect score: 2131

Sequence: 1 MQALVLLICALLGHSSCQ.....RDTDTGALLFIGKILDRPGP 418

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 1297172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2131	100.0	418	16	US-10-619-149-1
2	2125	99.7	418	12	Sequence 1, Appli
3	2125	99.7	418	14	Sequence 1, Appli
4	2125	99.7	418	15	Sequence 1, Appli
5	2125	99.7	418	15	Sequence 1, Appli
6	2106	98.8	418	12	Sequence 34, Appl
7	2097	98.4	418	14	Sequence 2, Appli
8	1870	87.8	379	14	Sequence 3, Appli
9	1789	84.0	418	15	Sequence 36, Appl
10	1784	83.7	362	9	Sequence 1, Appli
11	1538.5	25.3	360	12	Sequence 67, Appl
12	1538.5	25.3	360	15	Sequence 88, Appl
13	499	23.4	125	14	Sequence 84, Appl
14	458.5	21.5	377	10	Sequence 31, Appl
15	453.5	21.3	377	12	Sequence 66, Appl

16	453	21.3	371	15	US-10-023-634-87	Sequence 87, Appl
17	444	20.8	413	16	US-10-470-390A-38	Sequence 38, Appl
18	443	20.8	403	14	US-10-316-253-36	Sequence 36, Appl
19	432.5	20.3	503	14	US-10-025-514-8	Sequence 8, Appli
20	431	20.2	418	16	US-10-408-765A-2304	Sequence 2304, Ap
21	430	20.2	417	14	US-10-308-279-26	Sequence 26, Appl
22	430	20.2	417	16	US-10-624-631-23	Sequence 23, Appl
23	429	20.1	418	10	US-09-992-600A-92	Sequence 92, Appl
24	429	20.1	418	10	US-09-924-340-92	Sequence 92, Appl
25	429	20.1	418	10	US-09-992-095B-92	Sequence 92, Appl
26	429	20.1	418	10	US-09-999-570-92	Sequence 92, Appl
27	429	20.1	418	14	US-10-000-489-92	Sequence 92, Appl
28	429	20.1	418	14	US-10-000-986-92	Sequence 92, Appl
29	429	20.1	418	14	US-10-154-678-92	Sequence 92, Appl
30	427	20.0	418	12	US-10-411-037-22	Sequence 22, Appl
31	427	20.0	418	12	US-10-411-026-22	Sequence 22, Appl
32	427	20.0	418	14	US-10-097-340-286	Sequence 286, App
33	427	20.0	418	16	US-10-410-962-22	Sequence 22, Appl
34	427	20.0	418	16	US-10-411-049-22	Sequence 22, Appl
35	427	20.0	418	16	US-10-410-930-22	Sequence 22, Appl
36	427	20.0	418	16	US-10-410-997-22	Sequence 22, Appl
37	427	20.0	418	16	US-10-411-012-22	Sequence 22, Appl
38	427	20.0	418	16	US-10-287-994-22	Sequence 22, Appl
39	427	20.0	418	16	US-10-410-913-22	Sequence 22, Appl
40	426	20.0	522	14	US-10-025-514-14	Sequence 14, Appl
41	424	19.9	418	16	US-10-408-765A-54	Sequence 54, Appl
42	421	19.8	394	10	US-09-993-180-6	Sequence 6, Appli
43	421	19.8	394	14	US-10-025-514-2	Sequence 2, Appli
44	421	19.8	503	14	US-10-025-514-16	Sequence 16, Appl
45	421	19.8	522	14	US-10-025-514-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-10-619-149-1
; Sequence 1, Application US/10619149
; Publication NO. US20040161423A1
; GENERAL INFORMATION:
; APPLICANT: Valentis, Inc.
; APPLICANT: Kumar, Sanjeev M
; TITLE OF INVENTION: Polymer Modified Anti-Angiogenic Serpins
; FILE REFERENCE: 213-0086US
; CURRENT APPLICATION NUMBER: US/10/619,149
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 60/396,786
; PRIOR FILING DATE: 2002-07-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; TYPE: PRT
; LENGTH: 418
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Human PEDF
; LOCATION: (1)..(418)
; FEATURE:
; NAME/KEY: predicted signal sequence
; LOCATION: (1)..(20)
; OTHER INFORMATION: Cleavage site might be C or Q
; FEATURE:
; NAME/KEY: Predicted mature polypeptide
; LOCATION: (21)..(418)
; OTHER INFORMATION: Cleavage site might be C or Q, thus first amino acid might be Q
; OTHER INFORMATION: or N
; FEATURE:
; NAME/KEY: predicted neurotropic activity and receptor binding
; LOCATION: (88)..(121)
; FEATURE:
; NAME/KEY: collagen binding domain
; LOCATION: (134)..(163)
; FEATURE:

Db 181 NNWVQAQMGKGLARSTKEIPDEISILLGVAFHKGQWTVKFSRKTSLDFYLDERTVR 240
Qy 241 VPMMSDPKAVLYRGDLSCKIAQLPLTGSMSIIFPLKVTQNLTLIEESLTSEFIHD 300
Db 241 VPMMSDPKAVLYRGDLSCKIAQLPLTGSMSIIFPLKVTQNLTLIEESLTSEFIHD 300
Qy 301 IDRELKTVOAVLTVPKLSYEGVTKSLQEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
Db 301 IDRELKTVOAVLTVPKLSYEGVTKSLQEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
Qy 361 GFENWEDGAGTTPSPGLQPAHLTFPLDYHLNQPFIFVLRDITDGTGALLFIGKILDRPGP 418
Db 361 GFENWEDGAGTTPSPGLQPAHLTFPLDYHLNQPFIFVLRDITDGTGALLFIGKILDRPGP 418

RESULT 4
US-10-342-243-1
; Sequence 1, Application US/10342243
; Publication No. US20030216286A1
; GENERAL INFORMATION:
; APPLICANT: BOUCK, No. US20030216286A11
; APPLICANT: DAWSON, David
; APPLICANT: GILLIS, Paul
; APPLICANT: VOLPERT, Olga
; APPLICANT: CRAWFORD, Susan
; APPLICANT: STELLMACH, Veronica
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING ANGIOGENESIS
; FILE REFERENCE: 053662-5018-00
; CURRENT APPLICATION NUMBER: US/10/342,243
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: 09/122,079
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: PCT/US98/15228
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: 08/899,304
; PRIOR FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-342-243-1

Query Match 99.7%; Score 2125; DB 15; Length 418;
Best Local Similarity 99.5%; Pred. No. 3.2e-188;
Matches 416; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQALVLLCIGALGHSSCONPASPPEEGSPDPSTGALVEEEDPPFKVPVKNKLAASN 60
Db 1 MQALVLLCIGALGHSSCONPASPPEEGSPDPSTGALVEEEDPPFKVPVKNKLAASN 60
Qy 61 FGVDLYRVRSSMPTTNVLLSPLSVATALSALSGAERTESIIHRALYYDLISSPDING 120
Db 61 FGVDLYRVRSSMPTTNVLLSPLSVATALSALSGAERTESIIHRALYYDLISSPDING 120
Qy 121 TYKELLDTVTAPQKNLKSASRIVPEKLRKSSFVAPLEKSYGTRPVLVTGNPRLDLOEI 180
Db 121 TYKELLDTVTAPQKNLKSASRIVPEKLRKSSFVAPLEKSYGTRPVLVTGNPRLDLOEI 180
Qy 181 NNWVQAQMGKGLARSTKEIPDEISILLGVAFHKGQWTVKFSRKTSLDFYLDERTVR 240
Db 181 NNWVQAQMGKGLARSTKEIPDEISILLGVAFHKGQWTVKFSRKTSLDFYLDERTVR 240
Qy 241 VPMMSDPKAVLYRGDLSCKIAQLPLTGSMSIIFPLKVTQNLTLIEESLTSEFIHD 300
Db 241 VPMMSDPKAVLYRGDLSCKIAQLPLTGSMSIIFPLKVTQNLTLIEESLTSEFIHD 300
Qy 301 IDRELKTVOAVLTVPKLSYEGVTKSLQEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
Db 301 IDRELKTVOAVLTVPKLSYEGVTKSLQEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
Qy 361 GFENWEDGAGTTPSPGLQPAHLTFPLDYHLNQPFIFVLRDITDGTGALLFIGKILDRPGP 418
Db 361 GFENWEDGAGTTPSPGLQPAHLTFPLDYHLNQPFIFVLRDITDGTGALLFIGKILDRPGP 418

Db 361 GFENWEDGAGTTPSPGLQPAHLTFPLDYHLNQPFIFVLRDITDGTGALLFIGKILDRPGP 418

RESULT 5
US-10-603-387-1
; Sequence 1, Application US/10603387
; Publication No. US20040014664A1
; GENERAL INFORMATION:
; APPLICANT: BOUCK, No. US20040014664A11
; APPLICANT: DAWSON, David
; APPLICANT: GILLIS, Paul
; APPLICANT: VOLPERT, Olga
; APPLICANT: CRAWFORD, Susan
; APPLICANT: STELLMACH, Veronica
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING ANGIOGENESIS
; FILE REFERENCE: 053662-5018-00
; CURRENT APPLICATION NUMBER: US/10/603,387
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: 09/122,079
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: PCT/US98/15228
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: 08/899,304
; PRIOR FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-603-387-1

Query Match 99.7%; Score 2125; DB 15; Length 418;
Best Local Similarity 99.5%; Pred. No. 3.2e-188;
Matches 416; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQALVLLCIGALGHSSCONPASPPEEGSPDPSTGALVEEEDPPFKVPVKNKLAASN 60
Db 1 MQALVLLCIGALGHSSCONPASPPEEGSPDPSTGALVEEEDPPFKVPVKNKLAASN 60
Qy 61 FGVDLYRVRSSMPTTNVLLSPLSVATALSALSGAERTESIIHRALYYDLISSPDING 120
Db 61 FGVDLYRVRSSMPTTNVLLSPLSVATALSALSGAERTESIIHRALYYDLISSPDING 120
Qy 121 TYKELLDTVTAPQKNLKSASRIVPEKLRKSSFVAPLEKSYGTRPVLVTGNPRLDLOEI 180
Db 121 TYKELLDTVTAPQKNLKSASRIVPEKLRKSSFVAPLEKSYGTRPVLVTGNPRLDLOEI 180
Qy 181 NNWVQAQMGKGLARSTKEIPDEISILLGVAFHKGQWTVKFSRKTSLDFYLDERTVR 240
Db 181 NNWVQAQMGKGLARSTKEIPDEISILLGVAFHKGQWTVKFSRKTSLDFYLDERTVR 240
Qy 241 VPMMSDPKAVLYRGDLSCKIAQLPLTGSMSIIFPLKVTQNLTLIEESLTSEFIHD 300
Db 241 VPMMSDPKAVLYRGDLSCKIAQLPLTGSMSIIFPLKVTQNLTLIEESLTSEFIHD 300
Qy 301 IDRELKTVOAVLTVPKLSYEGVTKSLQEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
Db 301 IDRELKTVOAVLTVPKLSYEGVTKSLQEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
Qy 361 GFENWEDGAGTTPSPGLQPAHLTFPLDYHLNQPFIFVLRDITDGTGALLFIGKILDRPGP 418
Db 361 GFENWEDGAGTTPSPGLQPAHLTFPLDYHLNQPFIFVLRDITDGTGALLFIGKILDRPGP 418

RESULT 6
US-10-262-839-34
; Sequence 34, Application US/10262839
; Publication No. US2004003887A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John,
; APPLICANT: Anderson, David W.,

```

; APPLICANT: Boldog, Ferenc,
; APPLICANT: Burgess, Catherine,
; APPLICANT: Catterton, Elina,
; APPLICANT: Edinger, Shlomit,
; APPLICANT: Ellerman, Karen,
; APPLICANT: Gerlach, Valerie,
; APPLICANT: Gorman, Linda,
; APPLICANT: Guo, Xiaojia,
; APPLICANT: Ji, Weizhen,
; APPLICANT: Kekuda, Rameeh,
; APPLICANT: Leach, Martin,
; APPLICANT: Li, Li,
; APPLICANT: Miller, Charles,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Reiger, Daniel,
; APPLICANT: Rothenberg, Mark,
; APPLICANT: Shimkets, Richard,
; APPLICANT: Smithson, Glenda,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Taupier, Raymond, Jr.,
; APPLICANT: Vernet, Corine,
; APPLICANT: Voss, Edward,
; APPLICANT: Zerhusen, Brian,
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-462A
; CURRENT APPLICATION NUMBER: US/10/262,839
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,044
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,849
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/327,342
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/328,044
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,849
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/327,342
; PRIOR FILING DATE: 2002-04-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 34
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-262-839-34

Query Match          99.8%; Score 2106; DB 12; Length 418;
Best Local Similarity 99.0%; Pred. No. 1.8e-186;
Matches 414; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MQALVLLCIGALGHSCQNPASPPPEGSPDPDSTGALVEEDPPFKVPVKLAASVN 60
Db 1 MQALVLLCIGALGHSCQNPASPPPEGSPDPDSTGALVEEDPPFKVPVKLAASVN 60

Qy 61 FGDLVVRSSMSTPTNVLLSPVATALSALSGAEQRTESIHRALYYDLISSPDH 120
Db 61 FGDLVVRSSMSTPTNVLLSPVATALSALSGAEQRTESIHRALYYDLISSPDH 120

Qy 121 TYKELLDTVTAPQKNLSASRIKSSVAPLEKSYGTRPRVLTGNPRDLQEI 180
Db 121 TYKELLDTVTAPQKNLSASRIKSSVAPLEKSYGTRPRVLTGNPRDLQEI 180

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RESULT 7

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US-10-216-373-2
; Sequence 2, Application US/10216373
; Publication No. US20030096750A1
; GENERAL INFORMATION:
; APPLICANT: Tombran-Tink, Joyce
; APPLICANT: Steele, Fintan R
; APPLICANT: Chader, Gerald J
; APPLICANT: Becerra, Sofia P
; APPLICANT: Johnson, Lincoln V
; APPLICANT: Rodriguez, Ignacio R
; TITLE OF INVENTION: RETINAL PIGMENTED EPITHELIUM DERIVED NEUROTROPIC FACTOR
; FILE REFERENCE: 2026-4203US1
; CURRENT APPLICATION NUMBER: US/10/216,373
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/08/520,373
; PRIOR FILING DATE: 1995-08-29
; PRIOR APPLICATION NUMBER: 08/377,710
; PRIOR FILING DATE: 1995-01-25
; PRIOR APPLICATION NUMBER: 08/279,979
; PRIOR FILING DATE: 1994-07-25
; PRIOR APPLICATION NUMBER: 07/894,215
; PRIOR FILING DATE: 1992-06-04
; PRIOR APPLICATION NUMBER: 07/952,796
; PRIOR FILING DATE: 1992-09-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 418
; TYPE: PRT
; ORGANISM: HUMAN
; US-10-216-373-2

Query Match          98.4%; Score 2097; DB 14; Length 418;
Best Local Similarity 98.8%; Pred. No. 1.3e-185;
Matches 413; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MQALVLLCIGALGHSCQNPASPPPEGSPDPDSTGALVEEDPPFKVPVKLAASVN 60
Db 1 MQALVLLCIGALGHSCQNPASPPPEGSPDPDSTGALVEEDPPFKVPVKLAASVN 60

Qy 61 FGDLVVRSSMSTPTNVLLSPVATALSALSGAEQRTESIHRALYYDLISSPDH 120
Db 61 FGDLVVRSSMSTPTNVLLSPVATALSALSGAEQRTESIHRALYYDLISSPDH 120

Qy 121 TYKELLDTVTAPQKNLSASRIKSSVAPLEKSYGTRPRVLTGNPRDLQEI 180
Db 121 TYKELLDTVTAPQKNLSASRIKSSVAPLEKSYGTRPRVLTGNPRDLQEI 180

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QY 301 IDRELKTQAVLTVPKLSYEGETVKSLOEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
DB 301 IDRELKTQAVLTVPKLSYEGETVKSLOEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
QY 361 GFENWEDGAGTTSPGLQPAHLTFPLDYHLNQPFIFVLRDTDTGALLFTGKILDRGP 418
DB 361 GFENWEDGAGTTSPGLQPAHLTFPLDYHLNQPFIFVLRDTDTGALLFTGKILDRGP 418

RESULT 8
US-10-216-373-3
; Sequence 3, Application US/10216373
; Publication No. US20030096750A1
; GENERAL INFORMATION:
; APPLICANT: Tombran-Tink, Joyce
; APPLICANT: Steele, Fintan R
; APPLICANT: Chader, Gerald J
; APPLICANT: Becerra, Sofia P
; APPLICANT: Johnson, Lincoln V
; APPLICANT: Rodriguez, Ignacio R
; TITLE OF INVENTION: RETINAL PIGMENTED EPITHELIUM DERIVED NEUROTROPIC FACTOR
; FILE REFERENCE: 2026-4203US1
; CURRENT APPLICATION NUMBER: US/10/216,373
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/08/520,373
; PRIOR FILING DATE: 1995-08-29
; PRIOR APPLICATION NUMBER: 08/377,710
; PRIOR FILING DATE: 1995-01-25
; PRIOR APPLICATION NUMBER: 08/279,979
; PRIOR FILING DATE: 1994-07-25
; PRIOR APPLICATION NUMBER: 07/894,215
; PRIOR FILING DATE: 1992-06-04
; PRIOR APPLICATION NUMBER: 07/952,796
; PRIOR FILING DATE: 1992-09-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 379
; TYPE: PRT
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: /note= Met 1...Ile 4 is an N-terminal fusion to
; OTHER INFORMATION: Asp 44...Pro 418 of SEQ ID No. US20030096750A1 2; Met 1...Glu 43
; OTHER INFORMATION: of SEQ ID NO:2 is deleted
US-10-216-373-3

Query Match 87.8%; Score 1870; DB 14; Length 379;
Best Local Similarity 98.7%; Pred. No. 1.3e-164;
Matches 370; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 44 DPFKVPVKNLAAVSNFGDYLVRSMSPTTNVLLSPLSVATLSALSGAEQRTESI 103
DB 5 DPFKVPVKNLAAVSNFGKDLVRSMSPTTNVLLSPLSVATLSALSGAEQRTESI 64
QY 104 IHRALYYDLISSPDHGTXYKELDTVTAPQKNLKSASRIVFEEKLRKSSFVAPLEKSYG 163
DB 65 IHRALYYDLISSPDHGTXYKELDTVTAPQKNLKSASRIVFEEKLRKSSFVAPLEKSYG 124
QY 164 TRPVLGNRPDLQEQENNNVQAQMKGLARSTKEIPDEISILLGVAFKQGWTKFDS 223
DB 125 TRPVLGNRPDLQEQENNNVQAQMKGLARSTKEIPDEISILLGVAFKQGWTKFDS 184
QY 224 RKTSLDFYLDEERTVRPMMSPDKAVLRYGLSDLSCKIAQLPLTGSMSIIFFLPLKVT 283
DB 185 RKTSLDFYLDEERTVRPMMSPDKAVLRYGLSDLSCKIAQLPLTGSMSIIFFLPLKVT 244
QY 284 QNLTLIEESLTSSEIHDRELKTQAVLTVPKLSYEGETVKSLOEMKLSLFDSPDF 343
DB 245 QNLTLIEESLTSSEIHDRELKTQAVLTVPKLSYEGETVKSLOEMKLSLFDSPDF 304
QY 344 SKITGPKIKLTQVEHRA GFENWEDGAGTTSPGLQPAHLTFPLDYHLNQPFIFVLRDTDT 403

DB 305 SKITGPKIKLTQVEHRA GFENWEDGAGTTSPGLQPAHLTFPLDYHLNQPFIFVLRDTDT 364
QY 404 GALLFIGKILDRGP 418
DB 365 GALLFIGKILDRGP 379
RESULT 9
US-10-258-666-36
; Sequence 36, Application US/10258666
; Publication No. US20040005578A1
; GENERAL INFORMATION:
; APPLICANT: Yamada, Yoji
; APPLICANT: Sekine, Susumu
; APPLICANT: Kikuchi, Yasuhiro
; APPLICANT: Sakurada, Kazuhiro
; APPLICANT: Kyowa Hakkō Kogyo Co., Ltd.
; TITLE OF INVENTION: Myocardial Cell Proliferation-Associated Genes
; FILE REFERENCE: 082382-000000US
; CURRENT APPLICATION NUMBER: US/10/258,666
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: JP 2000-126741
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: WO PCT/JP01/03700
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: RHDH-140, PEDF
US-10-258-666-36

Query Match 84.0%; Score 1789; DB 15; Length 418;
Best Local Similarity 83.5%; Pred. No. 4.9e-157;
Matches 348; Conservative 36; Mismatches 23; Indels 4; Gaps 3;
QY 1 MQALLVLLCIGALLGHSSQON-PASPPPEGSDPDSTG-ALVVEEDPFKVPVKNLAAV 58
DB 1 MOTIVLLLTGALLGHSSQONVPS--SQDSPAPDSTGEPVVEEDPFKVPVKNLAAV 58
QY 59 SNFGDYLVRSMSPTTNVLLSPLSVATLSALSGAEQRTESIHRALYYDLISSPDI 118
DB 59 SNFGDYLVRSMSPTTNVLLSPLSVATLSALSGAEQRTESIHRALYYDLISSPDI 118
QY 119 HGTXYKELDTVTAPQKNLKSASRIVFEEKLRKSSFVAPLEKSYGTRPRVLTGNRDLQ 178
DB 119 HSTYKELASVTAPENKPKASRIVFEEKLRKSSFVAPLEKSYGTRPRVLTGNRDLQ 178
QY 179 EINNVMVQAQMKGLARSTKEIPDEISILLGVAFKQGWTKFDSRKTSLDFYLDEERT 238
DB 179 EINNVMVQAQMKGLARSTKEIPDEISILLGVAFKQGWTKFDSRKTSLDFYLDEERT 238
QY 239 VVPMSPDKAVLRYGLSDLSCKIAQLPLTGSMSIIFFLPLKVTQNLTLIEESLTSSEI 298
DB 239 VVPMSPDKAVLRYGLSDLSCKIAQLPLTGSMSIIFFLPLKVTQNLTLIEESLTSSEI 298
QY 299 HDIDRELKTQAVLTVPKLSYEGETVKSLOEMKLSLFDSPDFSKITGPKIKLTQVEH 358
DB 299 HDIDRELKTQAVLTVPKLSYEGETVKSLOEMKLSLFDSPDFSKITGPKIKLTQVEH 358
QY 359 RAGFENWEDGAGTTSPGLQPAHLTFPLDYHLNQPFIFVLRDTDTGALLFTGKILDP 415
DB 359 RAGFENWEDGAGTTSPGLQPAHLTFPLDYHLNQPFIFVLRDTDTGALLFTGKILDP 415
RESULT 10
US-09-875-114-1
; Sequence 1, Application US/09875114
; Patent No. US2002002131A1
; GENERAL INFORMATION:

APPLICANT: No. US200200002131althwestern University
APPLICANT: No. US200200002131althwestern University
APPLICANT: David Dawson
APPLICANT: Paul Gillis
TITLE OF INVENTION: Methods and Compositions for Inhibiting Angiogenesis
FILE REFERENCE: 0290-2302
CURRENT APPLICATION NUMBER: US/09/875,114
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 09/122,079
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: PCT/US98/15228
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: US 08/899,304
PRIOR FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 362
TYPE: PRT
ORGANISM: Homo sapiens
US-09-875-114-1

Query Match 83.7%; Score 1784; DB 9; Length 362;
Best Local Similarity 100.0%; Pred. No. 1.1e-156; Indels 0; Gaps 0;
Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQALVLLCTGALGHSSCONPSPPEEGSPDPSTGALVEEDPPFKVPVVKLAASVN 60
DB 1 MQALVLLCTGALGHSSCONPSPPEEGSPDPSTGALVEEDPPFKVPVVKLAASVN 60
QY 61 FGVDLYVRSSMPTTNVLLSPVATALSALSGAEQRTESIIRALYDILISSPDH 120
DB 61 FGVDLYVRSSMPTTNVLLSPVATALSALSGAEQRTESIIRALYDILISSPDH 120
QY 121 TYKELLDTVTAPQKLSASRIIVFEKLRKSSFVAPLEKSYGTRPRVLTGNPRDLQ 180
DB 121 TYKELLDTVTAPQKLSASRIIVFEKLRKSSFVAPLEKSYGTRPRVLTGNPRDLQ 180
QY 181 NNWVQAMKGLARSTKEIPDEISILLGVAFKQGWTKFDSRKTSLDFYLDERTVR 240
DB 181 NNWVQAMKGLARSTKEIPDEISILLGVAFKQGWTKFDSRKTSLDFYLDERTVR 240
QY 241 VPWMSDPKAVLYRGDLSCKIAQLPLTGSMSIIFFLPKVTQNTLTIIEESLTSF 300
DB 241 VPWMSDPKAVLYRGDLSCKIAQLPLTGSMSIIFFLPKVTQNTLTIIEESLTSF 300
QY 301 IDRELKTQVAVLTPVKLKSIEGEVTKSLQEMKLSLQSLFSDPSFKITGPKIK 355
DB 301 IDRELKTQVAVLTPVKLKSIEGEVTKSLQEMKLSLQSLFSDPSFKITGPKIK 355

RESULT 11
US-10-037-417-67
Sequence 67, Application US/10037417
Publication No. US20040052806A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaochong
APPLICANT: Spytak, Kimberly A
APPLICANT: Patturajan, Meera
APPLICANT: Grosse, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Vernet, Corine A.M.
APPLICANT: Li, Li
APPLICANT: Gorman, Linda
APPLICANT: Edinger, Shlomit R
APPLICANT: Sciorra, Paul
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M
APPLICANT: Rothenberg, Mark

APPLICANT: Stone, David J
APPLICANT: Boldog, Ferenc L
APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Anderson, David W
APPLICANT: Padigaru, Muralidhara
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Miller, Charles E
APPLICANT: Eisen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/10/037,417
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/303,231
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/305,050
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/318,405
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/318,700
NUMBER OF SEQ ID NOS: 227
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 67
LENGTH: 360
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Serpin
OTHER INFORMATION: Consensus Sequence
US-10-037-417-67

Query Match 25.3%; Score 538.5; DB 12; Length 360;
Best Local Similarity 33.6%; Pred. No. 4.7e-41;
Matches 122; Conservative 88; Mismatches 140; Indels 13; Gaps 9;

QY 63 YDLVVRSSMPTTNVLLSPVATALSALSGAEQRTESIIRALYDIL--ISSPDH 120
DB 1 FDYKELAKESPDKNIFPSPVISALAMLSLGAKGSTATQILEVLGNLTSETAD 60
QY 121 TYKELLDTVTAPQK--NLKSASRIIVFEKLRKSSFVAPLEKSYGTRPR-VLTGNPRDL 177
DB 61 GFQHLHLNRPDKLQKLTANALFVDKSLKLDSEFLVDKLYGAEVQSDSDAE 120
QY 178 -QEINNWNWQAMKGLARSTKEIPDEISILLGVAFKQGWTKFDSRKTSLDFYLD 236
DB 121 KKQINDWVKKTKQKIDKLLSDLPDTRVLVNAIVFKGKWKTFDPDPENTREDFYVDET 180
QY 237 RTVVRPNMSDPKAVLYRGDLSCKIAQLPLTGSMSIIFFLPKVTQNTLTIIEESLTS 296
DB 181 TTVKVPWMSQTGRFTRYGDEELNCQVLEFYKGNASMLILPDE--GGLETVERKALTPE 238
QY 297 FIHIDRELKTQVAVLTPVKLKSIEGEVTKSLQEMKLSLQSLF--DSPDFSKIT-GPKIK 354
DB 239 TLKKWTKSLTKRSVELYLPKFLKLEISYDLKDKVLEKLGITDLFSNKADLSGSDKOLKVS 298
QY 355 QVEHRACFEWNEDGAGTTSPG--LQPAHLTFDVLHNPFFVLRTDQDGLLPIGKI 412
DB 299 KVVHKAFLVNEEGTEAAATGVIIVRSLP-PPEFRANRPFLLIRDNPTGSLFWGKV 357
QY 413 LDP 415
DB 358 VNP 360

```

RESULT 12
US-10-023-634-88
; Sequence 88, Application US/10023634
; Publication No. US20030236389A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A
; APPLICANT: Colman, Steven D
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Ballinger, Robert A
; APPLICANT: Guo, Xiaojia
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Li, Li
; APPLICANT: Ellerman, Karen
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shomir R
; APPLICANT: Gangolli, Esha A
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Gerlach, Valerie
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; TITLE OF INVENTION: Using the Same
; FILE REFERENCE: 21402-221
; CURRENT APPLICATION NUMBER: US/10/023,634
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/256,025
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/265,163
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,929
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/274,864
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/276,688
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,880
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/286,409
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/309,246
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/315,600
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 360
; TYPE: PAT
; ORGANISM: Homo sapiens
US-10-023-634-88

Query Match 25.3%; Score 538.5; DB 15; Length 360;
Best Local Similarity 33.6%; Pred. No. 4.7e-41;
Matches 122; Conservative 88; Mismatches 140; Indels 13; Gaps 9;

QY 63 YDLVRRSSMPTTNVLLSPUSVATLSALSLGAEORTESIIRALYYDL--TSSPDHNG 120
:||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 1 FDLVRELAKESPDKNIFFPVSISALAMSLGAKGSTATQILEVGFNLTETSEADH 60
:||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:

QY 121 TYKLLDVTAPQK-NLKASRVFEKLRKIKSFVAPELKSXYGTRPR-VLTGPNRLDL 177
:||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 61 GFQHLHLNRPDNKILQKLTANALFVDSKLLDSFLEDVKLYGAEVQSDPSDAEEA 120
:||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:

QY 178 -QEINNWWQAQMKGLARSTKEIPDEISILLGVAFKQGWTKFDSRKTSLDFYLD 236

```

```

Db 121 KKQINDWVKKTKQKIDLLSDLPDTRLVNVAIYFKGKWTKFPDPENTREDFYVDET 180
:||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:

QY 237 RTVRPMMSDPKAVIRYGLDSDLSCKIAQLPLTGSMSIIFPLPKVTQNLTLIESLTSE 296
:||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 181 TTVKVPMMSTQGRTRYGRDEELNCQVLELPYKGNASMLIILPDE--GGLTETVSKALTPE 238
:||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:

QY 297 FIDIDRELKTVQAVLTVPKLKSVEGEVTKSLQEMKIQSLF-DSPDPFSKIT-GKPIKLT 354
:||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 239 TLKKWTKSLTKRSVELYLPKFKLEISYDLKDVLEKLGITDLFSNKADLSGISEDKDLKVS 298
:||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:

QY 355 QVEHRAGFEMNEDGAGITTPSPG--LQPAHLTFPLDYHLNQPFIFVLRTDPTGALLFIQKI 412
:||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 299 KVVHKAFLVNEEGTEAAATGVIIIPRSLP-PPEFKANRPFLLIIRNDNPTGSIILFMGKV 357
:||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:

QY 413 LDP 415
:||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 358 VNP 360
:||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:

RESULT 13
US-10-263-828-84
; Sequence 84, Application US/10263828
; Publication No. US20030138905A1
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; TITLE OF INVENTION: Compositions isolated from bovine
; TITLE OF INVENTION: mammary gland and methods for their use.
; FILE REFERENCE: 11000.1044Uicon
; CURRENT APPLICATION NUMBER: US/10/263,828
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 125
; TYPE: PAT
; ORGANISM: Bovine
US-10-263-828-84

Query Match 23.4%; Score 499; DB 14; Length 125;
Best Local Similarity 83.3%; Pred. No. 4.1e-38;
Matches 105; Conservative 3; Mismatches 16; Indels 2; Gaps 1;

QY 1 MQALVLLLCIGALLCHSSCONPASPPEGSDPDSTGALVEEDPFFKVPVKNLAAAVSN 60
:||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 1 MQALVLLMTGALLGFRCONAQO--EAGSLTPESTGAPVEEDPFFKVPVKNLAAAVSN 58
:||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:

QY 61 FGVDLYRVRSSMPTTNVLLSPUSVATLSALSLGAEORTESIIRALYYDLISSPDHNG 120
:||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 59 FGVDLYRVRSGESPTANVLLSPUSVATLSALSLGAEORTESIIRALYYDLISSPDHNG 118
:||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:

QY 121 TYKELL 126
:||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 119 TYKDLL 124
:||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:

RESULT 14
US-09-823-187-31
; Sequence 31, Application US/09823187
; Publication No. US20030096952A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Liu, Xiaohong
; APPLICANT: Majumder, Kumud
; APPLICANT: Padigaru, Muralidhar
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A
; APPLICANT: Spaderna, Steven X
; APPLICANT: Spytek, Kimberly

```

APPLICANT: Taupier, Raymond J
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-745
CURRENT APPLICATION NUMBER: US/09/823,187
CURRENT FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-04-05
PRIOR FILING DATE: 2000-04-05
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-10
PRIOR FILING DATE: 2000-04-10
PRIOR FILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 103
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
LENGTH: 377
TYPE: PRT
ORGANISM: Homo sapiens
US-09-823-187-31

Query Match 21.5%; Score 458.5; DB 10; Length 377;
Best Local Similarity 28.8%; Pred. No. 1.3e-33; Indels 25; Gaps 10;
Matches 113; Conservative 102; Mismatches 152;
QY 34 DSTGALVEEDPFFKVPVKNLAARVNFYDLYRVSSMSPTTNVLLSPLSVATLSALS 93
Db 1 DSSRAL-----KLASANADFAFSLYKELVEQNPDKNIFSPVSISSALAMLS 47
QY 94 LGAEQRTESIHEALYYDL--ISSPDHGTIKYKELLDTVTAPQKNLK--SASRIVFEKLR 149
Db 48 LGAGNTATQILEVGLFNLTETSEABHOGFOHLLQTLNRPDTGLQTLTGNALFVDSK 107
QY 150 IKSSFVAPLEKSYGTRP-RVLTGNPRDLQEIINNWTQAKMGKGLARSTKEIPDEISILL 208
Db 108 LLDEFLEDSKRLYQSEVFSVDFSDPEAKKQINDWVEKKTQGIKIDLLKDLSDTVLV 167
QY 209 GVAHFQGWTKEDSKTSLEDPYLBERTVRVPMMSDPKAVLRGLSDLSCKTAQPL 268
Db 168 NYTFYFGKWKPPDELTBEEDFHVDDKTVTKVPMNQ-LGTFYFPRDELNCKVLELPY 226
QY 269 TG-SMGIIFPLPKVTONLTIBESLTSBFHIDRELKTVQAVLTPVKLSYGEVTK 327
Db 227 KGNATSMFLPDEVCK-LEQVEAALSPTLKNLENMPREVELYLPKFSIECTYDLD 285
QY 328 SLOEMKQLSIF-DSPFSKIT-GKPKLTQVHRAGFEWNEGAGTTPSPG--LOPAHLT 383
Db 286 VLAKGITDLFSNQARLSGISEDEDLKSKAVHKAVLEVDDEEGTAAAAATGAIIVPS 345
QY 384 FPDYHNLNPFIFVLRTDTGALLFGKILDP 415
Db 346 PLEFTRADRPFLIYDNTGSIIFMGKVNP 377

RESULT 15

US-10-037-417-66
Sequence 66, Application US/10037417
Publication No. US20040052806A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Alsobrook II, John P

APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Patturajan, Meera
APPLICANT: Grosse, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Vernet, Corine A.M.
APPLICANT: Li, Li
APPLICANT: Gorman, Linda
APPLICANT: Edinger, Shlomit R
APPLICANT: Sciore, Paul
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M
APPLICANT: Rothenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Boldog, Ferenc L
APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Anderson, David W
APPLICANT: Padigaru, Muralidhara
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Miller, Charles E
APPLICANT: Eisen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/10/037,417
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/303,231
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/305,060
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/318,405
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/318,700
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 227
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 66
LENGTH: 377
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Serpin
OTHER INFORMATION: Consensus Sequence
US-10-037-417-66

Query Match 21.3%; Score 453.5; DB 12; Length 377;
Best Local Similarity 28.6%; Pred. No. 3.9e-33;
Matches 112; Conservative 102; Mismatches 153; Indels 25; Gaps 10;
QY 34 DSTGALVEEDPFFKVPVKNLAARVNFYDLYRVSSMSPTTNVLLSPLSVATLSALS 93
Db 1 DSSRAL-----KLASANADFAFSLYKELVEQNPDKNIFSPVSISSALAMLS 47
QY 94 LGAEQRTESIHEALYYDL--ISSPDHGTIKYKELLDTVTAPQKNLK--SASRIVFEKLR 149
Db 48 LGAGNTATQILEVGLFNLTETSEABHOGFOHLLQTLNRPDTGLQTLTGNALFVDSK 107
QY 150 IKSSFVAPLEKSYGTRP-RVLTGNPRDLQEIINNWTQAKMGKGLARSTKEIPDEISILL 208
Db 108 LLDEFLEDSKRLYQSEVFSVDFSDPEAKKQINDWVEKKTQGIKIDLLKDLSDTVLV 167

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2004, 11:09:24 ; Search time 40 Seconds
(without alignments)
1005.201 Million cell updates/sec

Title: US-10-619-149-1
Perfect score: 2131
Sequence: 1 MQALVLLICIGALLGHSSCO.....RDTDTGALLFIKILDPRGP 418

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 781*

1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2125	99.7	418	2 A47281	pigment epithelial
2	1827	85.7	359	2 A46046	serine proteinase
3	470	22.1	492	2 S43977	alpha-2-antiplasmi
4	466.5	21.9	491	2 S47217	alpha-2-antiplasmi
5	456.5	21.4	491	1 ITHUA2	alpha-2-antiplasmi
6	455	21.4	410	2 C39088	contrapsin precurs
7	448	21.0	405	2 A39088	alpha-1-antitropei
8	443	20.8	403	2 S08102	serine proteinase
9	430.5	20.2	416	2 B29131	kallikrein-binding
10	427	20.0	418	1 ITHU	alpha-1-antitrypsi
11	421.5	19.8	388	2 B39088	alpha-1-antitropei
12	420	19.7	418	2 JX0129	contrapsin precurs
13	419.5	19.7	418	1 S31507	serine proteinase
14	418	19.6	409	1 ITHA	alpha-1-antitrypsi
15	418	19.6	418	2 S23675	contrapsin-related
16	417	19.6	406	2 JX0346	alpha-1-antitropei
17	416.5	19.5	418	2 JH0494	alpha-1-antichymot
18	415.5	19.5	406	2 I53281	corticosteroid-bin
19	414	19.4	411	1 ITRT	alpha-1-antitrypsi
20	413	19.4	412	2 S31505	serine proteinase
21	408	19.1	413	2 JX0154	alpha-1-antitropei
22	405.5	19.0	413	2 I49474	alpha-1 proteinase
23	404	19.0	379	2 A42421	leukocyte elastase
24	403.5	18.9	408	2 S11320	serine proteinase
25	403	18.9	413	2 JX0267	alpha-1-antitropei
26	403	18.9	416	2 S21097	alpha-1-antitrypsi
27	403	18.9	417	2 S19724	kallikrein-binding
28	396	18.6	413	2 S54981	alpha-1-antitropei
29	395.5	18.6	413	2 I56481	alpha-1 proteinase

30 395.5 18.6 500 1 ITHUC1 complement C1 inh1
31 395 18.5 405 2 A28321 corticosteroid-bin
32 386 18.1 416 1 I7SH alpha-1-antitrypsi
33 384 18.0 413 2 A54968 alpha-1-antitrypsi
34 382 17.9 418 2 A39567 thyroxine-binding
35 381.5 17.9 410 2 A45457 alpha-1-proteinase
36 381.5 17.9 427 2 A49518 kallistatin precu
37 380.5 17.9 413 2 I49470 alpha-1 proteinase
38 380.5 17.9 413 2 I49452 alpha-1-antitrypsi
39 379 17.8 383 2 A36117 corticosteroid-bin
40 378.5 17.8 413 2 I49472 alpha-1 proteinase
41 378.5 17.8 413 2 S60036 alpha-1-antitrypsi
42 377.5 17.7 402 2 I49471 alpha-1 proteinase
43 377.5 17.7 433 1 ITHUC alpha-1 antichymot
44 377 17.7 430 2 A49190 corticosteroid-bin
45 375.5 17.6 413 2 I49473 alpha-1 proteinase

ALIGNMENTS

RESULT 1

A47281
pigment epithelial-differentiating factor precursor - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2003
R:Accession: A47281; S27967
R:Steele, F.R.; Chader, G.J.; Johnson, L.V.; Tombran-Tink, J.
Proc. Natl. Acad. Sci. U.S.A. 90, 1526-1530, 1993
A:Title: Pigment epithelium-derived factor: neurotrophic activity and identification as
submitted to the EMBL Data Library September 1991
A:Reference number: A47281; MUID:93165728; PMID:8434014
A:Accession: A47281
A>Status: Preliminary
A:Molecule type: DNA; protein
A:Residues: 1-418 <STE1>
A:Cross-references: GB:M76979; NID:G189777; PID:AAA60058.1; PID:G189778
A:Note: Sequence extracted from NCBI backbone (NCBIN:124952, NCBI:P:124953)
R:Steele, F.R.; Chader, G.J.; Johnson, L.V.; Tombran-Tink, J.
Submitted to the EMBL Data Library September 1991
A:Description: Pigment epithelium-differentiating factor (PEDF): Neurotrophic activity
ng.
A:Reference number: S27967
A:Accession: S27967
A:Molecule type: mRNA
A:Residues: 1-147,'X', 149-418 <STE2>
A:Cross-references: EMBL:M76979; NID:G189777
C:Genetics:
A:Gene: GDB:PEDF
A:Cross-references: GDB:138470; OMIM:172860
A:Map position: 17p13-17p13
C:Superfamily: Serpin
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-418/Product: pigment epithelial-differentiating factor #status predicted <MAT>

Query Match 99.7%; Score 2125; DB 2; Length 418;
Best Local Similarity 99.5%; Pred. No. 1.6e-149;
Matches 416; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQALVLLICIGALLGHSSCONPASPSPGSDPDSTGALVEEDPFKVPVKNKLAAYVN 60
Db 1 MQALVLLICIGALLGHSSCONPASPSPGSDPDSTGALVEEDPFKVPVKNKLAAYVN 60
QY 61 FGYDLYRVRSSMPTNNVLLSPLSVATALSALSGAEQRTESIIRALYDYLLISPDING 120
Db 61 FGYDLYRVRSSMPTNNVLLSPLSVATALSALSGADERTESIIRALYDYLLISPDING 120
QY 121 TYKEILDVTAPQKNLKSASRIVFEKKLRKSSFVAPLEKSYGTRPRVLTGNPRLDLOEI 180
Db 121 TYKEILDVTAPQKNLKSASRIVFEKKLRKSSFVAPLEKSYGTRPRVLTGNPRLDLOEI 180
QY 181 NNWVQAMQKGLARSTKEIPDEISILLGVAFHFGQWTKFDSRKTSLSEDFYLDERTVR 240
Db 181 NNWVQAMQKGLARSTKEIPDEISILLGVAFHFGQWTKFDSRKTSLSEDFYLDERTVR 240

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QY 241 VPMWDPKAVLYRGLDSDLSCKIAQLPLTGSMISIIFFLPKVTQNTLTLEESLTSEFIHD 300
Db 241 VPMWDPKAVLYRGLDSDLSCKIAQLPLTGSMISIIFFLPKVTQNTLTLEESLTSEFIHD 300
QY 301 IDRELKTVQAVLTVPKLSYEGEVTKSLQEMKLSQSLFSDPFSKITGPKIKLTQVEHRA 360
Db 301 IDRELKTVQAVLTVPKLSYEGEVTKSLQEMKLSQSLFSDPFSKITGPKIKLTQVEHRA 360
QY 361 GFENWEDGAGTTSPGLOPAHLTFPLDYHLNQPFIFVLRTDITGALLFTGKILDRGP 418
Db 361 GFENWEDGAGTTSPGLOPAHLTFPLDYHLNQPFIFVLRTDITGALLFTGKILDRGP 418

RESULT 2
A46046
serine proteinase inhibitor homolog EPC-1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2003
C;Accession: A46046
R;Pignolo, R.J.; Cristofalo, V.J.; Rotenberg, M.O.
J. Biol. Chem. 268: 8945-8957, 1993
A;Title: Senescent WI-38 cells fail to express EPC-1, a gene induced in young cells upon
A;Reference number: A46046; MUID:93232057; PMID:8473338
A;Accession: A46046
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-359 <PIG>
A;Experimental source: fetal lung-derived, fibroblast-like cells
A;Note: sequence extracted from NCBI backbone (NCBIP:129819)
C;Superfamily: Serpin

Query Match 85.7%; Score 1827; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 1.4e-127;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 NFGVLYRVSSMPTTNVLLSPLSVATLSALSGAEQRTESIHRALYDILSSPDH 119
Db 1 NFGVLYRVSSMPTTNVLLSPLSVATLSALSGAEQRTESIHRALYDILSSPDH 60
QY 120 GTYKELDTVAPQKLSASRIVFVKLRKSSFVAPLESYGTGPRVLTGNPRDLQ 179
Db 61 GTYKELDTVAPQKLSASRIVFVKLRKSSFVAPLESYGTGPRVLTGNPRDLQ 120
QY 180 INNWQAQMGKLSARSTKEIPDEISILLGVAFKQWTKFDSRKTSLDEYVLEERTV 239
Db 121 INNWQAQMGKLSARSTKEIPDEISILLGVAFKQWTKFDSRKTSLDEYVLEERTV 180
QY 240 RVPMSDPKAVLYRGLDSDLSCKIAQLPLTGSMISIIFFLPKVTQNTLTLEESLTSEFIH 299
Db 181 RVPMSDPKAVLYRGLDSDLSCKIAQLPLTGSMISIIFFLPKVTQNTLTLEESLTSEFIH 240
QY 300 DIDRELKTVQAVLTVPKLSYEGEVTKSLQEMKLSQSLFSDPFSKITGPKIKLTQVEH 359
Db 241 DIDRELKTVQAVLTVPKLSYEGEVTKSLQEMKLSQSLFSDPFSKITGPKIKLTQVEH 300
QY 360 AGFENWEDGAGTTSPGLOPAHLTFPLDYHLNQPFIFVLRTDITGALLFTGKILDRGP 418
Db 301 AGFENWEDGAGTTSPGLOPAHLTFPLDYHLNQPFIFVLRTDITGALLFTGKILDRGP 359

RESULT 3
S43977
alpha-2-antiplasmin precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Oct-1994 #sequence_revision 19-May-1995 #text_change 15-Sep-2003
C;Accession: S43977; S27260
R;Christensen, S.; Berglund, L.; Sottrup-Jensen, L.
FEBS Lett. 343, 223-228, 1994
A;Title: Primary structure of bovine alpha-2-antiplasmin.
A;Reference number: S43977; MUID:94229242; PMID:7513654
A;Accession: S43977
A;Molecule type: mRNA

us-10-619-149-1.rpr
```

```
A;Residues: 1-492 <CHR>
A;Cross-references: GB:X78436; NID:G498821; PIDN:CAA55200.1; PID:G498822
A;Experimental source: liver
R;Christensen, S.; Sottrup-Jensen, L.
FEBS Lett. 312, 100-104, 1992
A;Title: Bovine alpha(2)-antiplasmin. N-terminal and reactive site sequence.
A;Reference number: S27260; MUID:93050153; PMID:11385210
A;Accession: S27260
A;Molecule type: protein
A;Residues: 23-27,'O',29-39,'P',41-42,'E',44-45;374-415 <CH2>
C;Superfamily: Serpin
C;Keywords: Glycoprotein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-492/Product: alpha-2-antiplasmin #status predicted <MAT>
F;71-144/Disulfide bonds: #status experimental
F;127,249,296,310,317/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 22.1%; Score 470; DB 2; Length 492;
Best Local Similarity 30.2%; Pred. No. 6.2e-27;
Matches 120; Conservative 75; Mismatches 175; Indels 28; Gaps 7;

QY 22 PASPPPEEG--SPDPDSTGALVEEEDPPFKVFNKLAASVNFYDLYRVSSMPTTNVL 79
Db 64 PKKAPEDCKLSPTPEQT-----RELAPAMWTFITDLFSLVAQSTRPNLI 108
QY 80 LSPLSVATLSALSGAEQRTESIHRALYDILSSPDHITGKELDTVAPQKLSA 139
Db 109 LSPLSVALALSHLAGAQNQLQRLKEVLHAD--SGCLPHLLSRCLQDGLPGAFRL--A 164
QY 140 SRIVFEKRLKIKSSFVAPLESYGTGPRVLTGNPRDLQINNWQAQMGKLSARSTKEI 199
Db 165 ARMYLQKFPFKEDFLEQSEQLFGAKPMSLTGKMGEDLANINWVKEATGKIEDFLSDL 224
QY 200 PDETSILLGVAFKQWTKFDSRKTSLDEYVLEERTVVRPMNSDPKAVLYRGLDSDL 259
Db 225 PDDTVLLLLNAIHFGQFWRSKFDPNLTQCGAFHLDQFTVFVDMQALTYPLHFWLLEQ 284
QY 260 SCTIAQLPLTGSMISIIFFLPKVTQNTLTLEESLTSEFIHDIDRELKTVQAVLTVPK 319
Db 285 EIQAHPFVKNNMSFVLMPTREFWASQVLANLTWDLH--QPSLSERTKYQLPKLHL 342
QY 320 SYEGEVTKSLQEMKLSQSLFSDPFSKITGPKIKLTQVEHRAGFENWEDG--AGTTPSPGL 377
Db 343 KYQLDVLATLSQLGLQELFQAPDLRGISDERLVSVVQHSQSALELSAGVQAAAAATSTAM 402
QY 378 QPAHLTFPLDYHLNQPFIFVLRTDITGALLFTGKILDRP 415
Db 403 SRMSLS---SFIVNRPFLFFILEDSTSLPLFVGSVRNP 437

RESULT 4
S47217
alpha-2-antiplasmin - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Sep-2003
C;Accession: S47217; S48204
R;Menoud, P.A.; Sappino, N.; Boudal-Khosbeeni, M.; Vassalli, J.D.; Sappino, A.P.
submitted to the EMBL Data Library, August 1994
A;Description: The murine kidney is a major source of alpha 2-antiplasmin production.
A;Reference number: S47217
A;Accession: S47217
A;Molecule type: mRNA
A;Residues: 1-491 <MEN>
A;Cross-references: EMBL:Z36774; NID:G534037; PIDN:CRA85350.1; PID:G534038
R;Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
Eur. J. Biochem. 224, 863-871, 1994
A;Title: Characterization of the murine plasma fibrinolytic system.
A;Reference number: S48202; MUID:95010076; PMID:7523120
A;Accession: S48204
A;Molecule type: protein
A;Residues: 28-33 <LIJ>
C;Superfamily: Serpin
```


Query Match 21.9%; Score 466.5; DB 2; Length 491;
Best Local Similarity 31.7%; Pred. No. 1.1e-26;
Matches 116; Conservative 75; Mismatches 162; Indels 13; Gaps 5;

QY 53 KLAAVSNFGVDLYRVRSSMPTTNVLLSPLSVAATLALSGLGAORTESIIRALYYDL 112
:
Db 81 RLACAMWAFTTDLSLVAAQTSTSSNLVSLPSVALALSHLAGAQNQLHSLRVLHMT 140
:
QY 113 ISS-PDIHGTYKELLDTVTAPQKNLKASRIIVFEKKLRIKGSFVAPLEKSQTRPRVLTG 171
:
Db 141 GSCILPHLLSHFYQNLGPGT-----IRLAARIYLQKGFTTKDDFLQCSESLFGAKPVKLGT 195
:
QY 172 NPLDLQSINNVOAQMKLARSKEIPDEISILLGVAHFKGOWTKFSSEKTSLDFP 231
:
Db 196 KOEBEDLANINQWKEATEGKIETDFUSELPDSTVLULLNAIHFGHWRTKFDLSLTQKOFF 255
:
QY 232 YLDERTVRVPMSPDKAVLRIGLDSDLSCKIAQLPLTGSMSIIFFLPKVKTONLTLEE 291
:
Db 256 HLDERTVSVDMHAHSVPLRWLFLEQPEIQVAHFPPKNNMSFVVVMPTYPEWNVSEVLA 315
:
QY 292 SLTSEFIHDIRELKTQAVLTVPKLKLSYGEVTKSLQEMKLOSLFPSPDPSEKITGPPI 351
:
Db 316 NLTWDTLYHPBSLOBREPTKWNL--PKHLQQQLDVLVATLSLQGLQELFOGPDLRGISQNL 373
:
QY 352 KLTOVEHRAGFEWNEDG--AGTTPSGIQAHLTFPLDYHLNQPPIFVLRDITDTCALLPI 409
:
Db 374 WVSSVQHQSITSELSEAGVEAAAATSVANRMSSL---SFTVNRPLFITMEDTICGPLFV 430
:
QY 410 GKILD P 415
:
Db 431 GSRNP 436

RESULT 5
ITHUA2
alpha-2-antiplasmin precursor [validated] - human
N/Alternate names: alpha-2-fi; alpha-2-plasmin inhibitor precursor
C/Species: Homo sapiens (man)
C/Date: 31-Jul-1989 #sequence revision 12-Apr-1996 #text change 15-Sep-2003
C/Accession: A31402; A32163; A41504; A26684; A24708; PC2129; S00068; S32524; S32529
R/Hiroawa, S.; Nakamura, Y.; Miura, O.; Sumi, Y.; Aoki, N.
Proc. Natl. Acad. Sci. U.S.A. 85, 6836-6840, 1988
A/Title: Organization of the human alpha-2-plasmin inhibitor gene.
A/Reference number: A31402; MUID:88320531; PMID:3166140
A/Accession: A31402
A/Molecule type: DNA
A/Residues: 1-491 <HIR>
A/Cross-references: GB:M20786; GB:J03830; NID:g177884; PIDN:AAA51554.1; PID:g177886
R/Hiroawa, S.; Nakamura, Y.; Miura, O.; Sumi, Y.; Aoki, N.
Proc. Natl. Acad. Sci. U.S.A. 86, 1612-1613, 1989
A/Reference number: A32163
A/Accession: A32163
A/Status: not compared with conceptual translation
A/Molecule type: DNA
R/Tone, M.; Kikuno, R.; Kume-Iwaki, A.; Hashimoto-Gotoh, T.
J. Biochem. 102, 1033-1041, 1987
A/Title: Structure of human alpha-2-plasmin inhibitor deduced from the cDNA sequence
A/Reference number: A41504; MUID:88139254; PMID:2830248
A/Accession: A41504
A/Molecule type: mRNA
A/Residues: 1-32 'W', 34-491 <TON>
A/Cross-references: GB:D00174; NID:g219409; PIDN:BAA00124.1; PID:g219410
R/Holmes, W.E.; Nelles, L.; Litjens, H.R.; Collen, D.
J. Biol. Chem. 262, 1659-1664, 1987
A/Title: Primary structure of human alpha-2-antiplasmin, a serine protease inhibitor
A/Reference number: A26684; MUID:87109313; PMID:2433286
A/Accession: A26684
A/Molecule type: mRNA
A/Residues: 4-288, 'D', 290-491 <HOL>
A/Cross-references: GB:J02654; NID:g178750; PIDN:AAA35543.1; PID:g178751
A/Note: the authors translated the codon GAR for residue 289 as His
R/Sumi, Y.; Nakamura, Y.; Aoki, N.; Sakai, M.; Muramatsu, M.

F:404/Inhibitory site: Met (chymotrypsin) #status predicted
F:437/Binding site: carbohydrate (Asn) #status absent

Query Match 21.4%; Score 456.5; DB 1; Length 491;
Best Local Similarity 28.4%; Pred. NO. 6.2e-26;
Matches 127; Conservative 86; Mismatches 181; Indels 53

Qy	5	VLLLCIGALLGHSSCONPAS-----PPEE-----GSDPDPOSTGNL--39
Dd	7	LVLVSNWSCLOQPCCSVFSEVSAMEPLGRQLTSGNQEQVSPLLLKLGNOBEPGGQTALKSP66
Qy	40	--VEBEDPFKKVP--VNKLAAAVNFGYDYLYRVRRSSMPTTNVLLSPLSVATAALSISLG95
Dd	67	PGVCSDRP---TPEOTHELARAMMAFTADLFSLVAOITSTCPNLILSPLSVALASHLAG123
Qy	96	AB-----QRTESIHRALYYDILISSPDTHGTGYKELLDTVTAPQXNKLKSASRIVFEEKLRK151
Dd	124	AQNHTLORLOQVLHAG-----SGPCFLPHLLSRLOCGLGPAPRL--AARMYLOKGFFTK175
Qy	152	SSEFVAPLEKSYCTRPRVLITGNPRLDQEIINNWOCAQMKGKLARSTKEIPDEISILLGWA211
Dd	176	EDFLSQSOLFGAKFSVUTGOEDDLANIQWKEATEGKIQFSLGFEDTVLLLLNAI235
Qy	212	HPFKGWVTFKDSRKTSLBDFYLDBERTVRVPMASDPKAVLYRGDLSJCKIAQLPTGS271
Dd	236	HFCGFWRNKFDPSSLTORQDSFHLDQSFVPVENMQARTYPLRWELLBQQEPIQVAHFPPKN295
Qy	272	NSIIIFLPKVTQNTLIEESLTSEPTH----TDRELKTVQAVLVTPVKULSYEEGVTKS328
Dd	296	NSGFVVLVPTHEWNYSQVLANLSWDTHLPLVMERPDK-----VRUPKPLYLKHOMDLVAT350
Qy	329	LOEMKLQSLFDPSDFSKITGPIKLTOVEHRAGFEWNEDGAGTTSPGPLQAHLVFPILDY388
Dd	351	LSQLGQELFQAPDDURGHISEQSLVVGVOQOSTLEUSEVGEAAAAATSTAMSEMLS-SF409
Qy	389	HUNQPFIVFLRDSTDGALLFGKILDP415
Dd	410	SVNRPFLEFIEDDTTGLPLFVSGVRNP436

RESULT 6
C39088
contrapsin precursor - guinea pig
C:Species: Cavia porcellus (guinea pig)
C:date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 15-Sep-2003
C:Accession: C39088
R:Suzuki, Y.; Yoshida, K.; Honda, E.; Sinchara, H.
J. Biol. Chem. 266: 928-932, 1991
A:title: Molecular cloning and sequence analysis of cDNAs coding for guinea pig alpha-1
A:reference_number: A39088; MUID:91093294; PMID:1985973
A:Accession: C39088
A:status: preliminary
A:molecule_type: mRNA
A:residues: 1-410 <SUZ>
A:cross-references: GB:M38573
C:superfamily: Serpin

Query Match	21.4%;	Score 455;	DB 2;	Length 410;
Best Local Similarity	28.1%;	Pred. No. 6e-26;		
Matches 111:	Conservative 101;	Mismatches 159;	Indels 24;	Gaps 9;

[illegible]

	QY	208	LGVAFKGGWVTKFDGRKTSLEDIFYLDEERTVEVPMMSDPKAVLRGCLDSDLCKIAQ--	265
			: : : : : : : : : : : : : :	
	Db	201	VNYIFRFGWEKFDPVKHTTQEDFHDANTTVKPVMKK-----QQOMHKAFHCSTIIQS	254
			: : : : : : : : : : : : : :	
	QY	266	--LPLTGMSIIEFFFLPKVTQNLTILIESLTSEFIHIDRELKTVOAVLTPKLKLSYE	322
			: : : : :~::~ : :~:: : :~:: : :~:: : :~:: : :	
	Db	255	VLLLDVEGNVTALFLPDE--GMQHLEETILTLPVFKFLRKTTWPAYVSLPKLSISGT	312
			: : : : :~::~ : :~:: : :~:: : :~:: : :~:: : :	
	QY	323	GEVTKSLOMKMQLSPD-SPDFSKIT-GPKIKUTQVEHRAGFEWNEDCAGTTSPGLQPA	380
			::: :~:: :~:: :~:: :~:: :~:: :~:: :~:: :~:: :~:: :~:: :~:: :~:: :	
	Db	313	YDLKEVLRDIGITNVFSGAADLSGITEDMPLKISKGLHALLTIDEGTEAAATAATVLEAT	372
			: : :~:: :~:: :~:: :~:: :~:: :~:: :~:: :~:: :~:: :~:: :~:: :~:: :	
	QY	381	HLTFPLDYHLNQPFIVLRTDTGALLFGIKILD	415
			: :~:: :~:: :~:: :~:: :~:: :~:: :~:: :~:: :~:: :~:: :~:: :~:: :	
	Db	373	RTRAPPRLFENKPEFFELIIDHSITDPLFVGKWMDP	407
			: :~:: :~:: :~:: :~:: :~:: :~:: :~:: :~:: :~:: :~:: :~:: :~:: :	

RESULT 7
A39088 alpha-1-antiproteinase S precursor - guinea pig
C:Species: Cavia porcellus (guinea pig)
C>Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 15-Sep-2003
C:Accession: A39088 R;Suzuki, Y.; Yoshida, K.; Honda, E.; Sinohara, H.
J. Biol. Chem. 266, 928-932, 1991
A:Title: Molecular cloning and sequence analysis of cDNAs coding for guinea pig alpha-1-
A:Reference number: A39088; MUID:91093294; PMID:1985973
A:Accession: A39088
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-405 <SUZ>
A:Cross-references: GB:M38571
C:Superfamily: Serpin

Query Match 21.0%; Score 448; DB 2; Length 405;
Best Local Similarity 28.3%; Pred. NO. 2e-25;
Matches 110: Conservative 98; Mismatches 161; Indels 20; Gaps 8;

QY	39	LVEEDPFFKVPVNVKALAAAVSNFGVDLYVRVRSSMSPPTNVLLSPLSVATALSLSLGAEB	98
Db	22	IWAEDAQAQVQSPSQIQPSLAHFAHSMYRVLTQCSNTSNIFSPSVSTATALAMVSVGAKG	81
QY	99	RTESIIRHALYYDL--ISSPDHGTXYKELDLTVTAP--QKNLKASASRIVEFKKLRIKSSP	154
Db	82	DHTQILRGLSFNLTEIAEADIHNGQLHGLTLNRPHSEHQLTTNGSLFDQQLKUKEXF	141
QY	155	VAPLEKSYGTRPRVLVT-GNPRLDQLEINWYQAQMKGLARSTKEIPEDEISILLGVAHF	213
Db	142	SEDVKTLYHAZAFPNFNSPKAEKQINAYVEKGTQGIVDLVKDLSDATVLAVNVYFF	201
QY	214	KQWTKTSDSRKTSILEDYLDDEETRVVPMMSDKPVLRYGLDSDLSCKIAQ-----LPL	268
Db	202	RKGWKEPFDVXHTTQEDPHVDVTSTTVKVPMMK-----REGKYAFHCSTIQSVLLLDY	255
QY	269	TGSMIIIFPLKVTQNTLTLSEISITSEFTHDIDRELKTVQAVLTVPKLKSVEGEVTKS	328
Db	256	EGNVATLFLLPDEE--GRQWHEETITTELIFKFKARKTERFANVHLPKLSISGTYDLKEV	313
QY	329	LQEMKLQSLF-DSPDFSKITGK-PIKLTQVHEHRAGFEWNEDGAGTTPSPGLQPAHLTFPL	386
Db	314	LGLHGIITNVFSDAADLSGVTEDIPLKISKGLHKALLTIDKGTGAAGATWVEFMPMSLPE	373
QY	387	DVHLNQPIFVLRDPTDTCALLFGIKILDP	415
Db	374	DL-SFNKPLFLIIIDHSTDTPLFVGVKMDP	402

RESULT 8
S08102
serine proteinase inhibitor 1 - rat
N;alternate names: growth hormone-induced proteinase inhibitor
C;Species: Rattus norvegicus (Norway rat)
C;date: 07-Sep-1990 #sequence revision 07-Sep-1990 #text change 15-Sep-2003

C;Accession: S08102; S11318; A29131
R;le Cam, A.
Submitted to the EMBL Data Library, August 1989
A;Reference number: S08099
A;Accession: S08102
A;Molecule type: mRNA
A;Residues: 1-403 <LEC>
A;Cross-references: EMBL:X16357; NID:G57230; PIDN:CAA34406.1; PID:G57231
R;Pages, G.; Rouayrenc, J.F.; le Cam, G.; Mariller, M.; le Cam, A.
Eur. J. Biochem. 190, 385-391, 1990
A;Title: Molecular characterization of three rat liver serine-protease inhibitors affected by rat hepatocytes: cDNA
A;Reference number: S11318; MUID:90306038; PMID:1694763
A;Accession: S11318
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-403 <PAG>
A;Cross-references: EMBL:X16357; NID:G57230; PIDN:CAA34406.1; PID:G57231
R;Yoon, J.B.; Towle, H.C.; Seelig, S.
J. Biol. Chem. 262, 4284-4289, 1987
A;Title: Growth hormone induces two mRNA species of the serine protease inhibitor gene 4
A;Reference number: A92632; MUID:87166046; PMID:3494016
A;Accession: A29131
A;Molecule type: mRNA
A;Residues: 82-234, 'L', 236-403 <YOO>
A;Cross-references: GB:M15917; GB:J02692; NID:G207041; PIDN:AAA42172.1; PID:G207042
C;Superfamily: Serpin

Query Match 20.8%; Score 443; DB 2; Length 403;
Best Local Similarity 30.5%; Pred. No. 4.5e-25;
Matches 113; Conservative 82; Mismatches 166; Indels 10; Gaps 7;

QY 54 LAAAVSFGDLYRVSRMSPTTNVLLSPVATLSALSGABQRTESIHRALYYDL- 112
DB 35 LASNTDFALSLYKLLALRNPDKNVFSPISIALTILSLGAKDSTMBEILGLKFNLT 94

QY 113 -ISSPDINGTYKELDDTVAP--QKNLKSASRIYFEKKLRIKSFVAPLEKSYGTRPRVL 169
DB 95 EITEEIHQGFHLLQSLQSDQVEINTGSALPIDKEQPISEFQSKTRALYQAEAFIA 154

QY 170 T-GNPRDLQEIINNVAQMKGLARSTKEIPDEISILLGVAFHFGQWTKYDSKTSLS 228
DB 155 DFKQPNBAKLLINDVSNQGTQKLAELFSLDEESTSVLVNLLFKGKVKVPNPNDTPE 214

QY 229 EDFYLDERTVVRPMWDPKAVLYGLDLSLSCKIAQLPTLGTMSIIFFLPKVTQNLTL 288
DB 215 SEFYLDKRSVKVPMWKEVTTTPYVDELSLCSVLELKYTGNASALFILPDQ--GKMQQ 272

QY 289 IEESLTSEFIHD-IDRELKTVQAVLTVPKJLKSVEGEVTKSLQEMKLSLF-DSPDPSKI 346
DB 273 VESSLOPETLKKWDXSLIPRIINDLRMPKFTSISTDYSLKEVLPBLGIGIKVFSQQAQLSRI 332

QY 347 TG-KPIKLTQVEHRAGFEWEDGAGTTPSPQLQPAHLTFPLDYLHNLQPFIFVLRLDTGA 405
DB 333 TGTDLVYSQVWKAVDVDBTGTEATAGVATVIRQRTLNFNFPFWVITDMSQS 392

QY 406 LLFYGKILDP 416
DB 393 ILFVAKITNPK 403

RESULT 9
B29131
Kallikrein-binding protein precursor - rat
N;Alternate names: contraptasin-like protease
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1989 sequence revision 31-Mar-1989 #text change 15-Sep-2003
C;Accession: B29131; A29448; S11319; JN0106; A40810; A37889; JX0156; S08039; S08101
R;Yoon, J.B.; Towle, H.C.; Seelig, S.
J. Biol. Chem. 262, 4284-4289, 1987
A;Title: Growth hormone induces two mRNA species of the serine protease inhibitor gene 4
A;Reference number: A92632; MUID:87166046; PMID:3494016
A;Accession: B29131
A;Molecule type: mRNA

A;Residues: 1-416 <YOO>
A;Cross-references: GB:M15916; GB:J02692; NID:G207043; PIDN:AAA42173.1; PID:G207044
R;le Cam, A.; Pages, G.; Auberger, P.; le Cam, G.; Leopold, P.; Benatrous, R.; Glaichenh
EMBO J. 6, 1225-1232, 1987
A;Title: Study of a growth hormone-regulated protein secreted by rat hepatocytes: cDNA
A;Reference number: A29448; MUID:87275813; PMID:2440672
A;Accession: A29448
A;Molecule type: mRNA
A;Residues: 1-97, 'V', 99-416 <LEC>
R;Pages, G.; Rouayrenc, J.F.; le Cam, G.; Mariller, M.; le Cam, A.
Eur. J. Biochem. 190, 385-391, 1990
A;Title: Molecular characterization of three rat liver serine-protease inhibitors affected by rat hepatocytes: cDNA
A;Reference number: S11318; MUID:90306038; PMID:1694763
A;Accession: S11319
A;Molecule type: mRNA
A;Residues: 11-97, 'V', 99-112, 'H', 113-386, 'P', 388-416 <PAG>
A;Cross-references: EMBL:X16358; NID:G57232; PIDN:CAA34407.1; PID:G57233
R;Pages, G.; Rouayrenc, J.F.; Rossi, V.; le Cam, G.; Mariller, M.; Szpirer, J.; Szpirer
Gene 94, 273-282, 1990
A;Title: Primary structure and assignment to chromosome 6 of three related rat genes en
A;Reference number: JN0106; MUID:91078650; PMID:2258058
A;Accession: JN0106
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 11-97, 'V', 99-325, 'D', 327-416 <PA2>
A;Cross-references: GB:X16362; NID:G57236; PIDN:CAA34409.1; PID:G57237
A;Experimental source: liver
R;Chai, K.X.; Ma, J.X.; Murray, S.R.; Chao, J.; Chao, L.
J. Biol. Chem. 266, 16029-16036, 1991
A;Title: Molecular cloning and analysis of the rat kallikrein-binding protein gene.
A;Reference number: A40810; MUID:91340751; PMID:1874745
A;Accession: A40810
A;Molecule type: DNA
A;Residues: 1-55, 'L', 53-97, 'V', 99-416 <CHA>
A;Cross-references: GB:IM67496
A;Note: the authors translated the codon CTC for residue 52 as Phe
R;Chao, J.; Chai, K.X.; Chen, L.M.; Xiong, W.; Chao, S.; Woodley-Miller, C.; Wang, L.;
J. Biol. Chem. 265, 16394-16401, 1990
A;Title: Tissue kallikrein-binding protein is a serpin. Purification, characterization,
A;Reference number: A37889; MUID:90375506; PMID:2398056
A;Accession: A37889
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr
A;Molecule type: mRNA
A;Residues: 1-49 <CH2>
R;Ohkubo, K.; Ogata, S.; Misumi, Y.; Takami, N.; Ikehara, Y.
J. Biochem. 109, 243-250, 1991
A;Title: Molecular cloning and characterization of rat contraptasin-like protease inhibit
A;Reference number: JX0156; MUID:91324305; PMID:1864837
A;Accession: JX0156
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-69, 'C', 71-72, 'A', 74-193, 'D', 195-249, 'V', 251-384, 'V', 386-416 <OHK>
C;Genetics:
A;Introns: 211/1; 302/2; 352/3
C;Superfamily: Serpin
C;Keywords: glycoprotein; serine proteinase inhibitor

Query Match 20.2%; Score 430.5; DB 2; Length 416;
Best Local Similarity 30.5%; Pred. No. 4e-24;
Matches 116; Conservative 80; Mismatches 157; Indels 27; Gaps 10;

QY 54 LAAAVSFGDLYRVSRMSPTTNVLLSPVATLSALSGABQRTESIHRALYYDL- 112
DB 45 LASINTDFSLYKLLALRNPDKNVFSPISIALAILSLGAKDSTMBEILGLKFNLT 104

QY 113 -ISSPDINGTYKELDDTVAP--QKNLKSASRIYFEKKLRIKSFVAPLEKSYGTRPRVL 169
DB 105 EITEEIHQGFHLLQSLQSDQVEINTGSALPIDKEQPISEFQSKTRALYQAEAFV- 163

QY 170 TGNPRDLQEIINNVAQMKGLARSTKEIPDEISILLGVAFHFGQWTKYD 222
DB 164 -----ADFKQCNEAKKFINVYSNQTQKIAELFSELQBERTSMVLVNVLLFKGKVKVPFN 218

A;Residues: 196-225 <LE12>
A;Cross-references: GB:J00066; NID:g177819; PIDN:AAB59370.1; PID:g177823
R;Chang, W.S.W.; Wardell, M.R.; Lomas, D.A.; Carrell, R.W.
Biochem. J. 314, 647-653, 1996
A;Title: Probing serpin reactive-loop conformations by proteolytic cleavage.
A;Reference number: S63599; MUID:96239126; PMID:8670081
A;Accession: S63599
A;Molecule type: protein
A;Residues: 371-385 <CHA>
R;Coutelle, C.; Speer, A.; Rogers, J.; Kalsheker, N.; Humphries, S.; Williamsen, R.
Biomed. Biochim. Acta 44, 421-431, 1985
A;Title: Construction and partial characterization of a human liver cDNA library.
A;Reference number: I39370; MUID:85225507; PMID:3873938
A;Accession: I39370
A;Status: preliminary; translated from GB/EMBL/DBDJB
A;Molecule type: mRNA
A;Residues: 387-399, 'D', 401-418 <COU>
A;Cross-references: GB:M26123; NID:g177815; PIDN:AAAS1545.1; PID:g177816
R;Faber, J.P.; Weidinger, S.; Olek, K.
Am. J. Hum. Genet. 46, 1158-1162, 1990
A;Title: Sequence data of the rare deficient alpha-1-antitrypsin variant PI Zausburg.
A;Reference number: A35338; MUID:90252805; PMID:2339709
A;Accession: A35338
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 122-124, 'H', 126-128; 363-365, 'K', 367-369 <FAB>
A;Experimental source: mutant PI Zausberg
A;Note: this Z mutation with Lys-366 arose from the M2 variant with His-125
R;Loebermann, H.; Tokuko, R.; Deisenhofer, J.; Huber, R.
submitted to the Brookhaven Protein Data Bank, September 1988
A;Reference number: A50775; PDB:7AP1
A;Contents: annotation; X-ray crystallography, 3.0 angstroms, tetragonal form 1, residue
R;Loebermann, H.; Tokuko, R.; Deisenhofer, J.; Huber, R.
submitted to the Brookhaven Protein Data Bank, September 1988
A;Reference number: A50794; PDB:8AP1
A;Contents: annotation; X-ray crystallography, 3.1 angstroms, hexagonal form, residues 4
R;Loebermann, H.; Tokuko, R.; Deisenhofer, J.; Huber, R.
submitted to the Brookhaven Protein Data Bank, September 1988
A;Reference number: A50810; PDB:9AP1
A;Contents: annotation; X-ray crystallography, 3.0 angstroms, tetragonal form 2, residue
R;Loebermann, H.; Tokuko, R.; Deisenhofer, J.; Huber, R.
J. Mol. Biol. 177, 531-556, 1984
A;Title: Human alpha-1-proteinase inhibitor. Crystal structure analysis of two crystal
A;Reference number: A58525; MUID:84292309; PMID:6332197
A;Contents: annotation; X-ray crystallography, 3.0 angstroms
R;Carrell, R.W.; Jeppsson, J.O.; Vaughan, L.; Brennan, S.O.; Owen, M.C.; Boswell, D.R.
FEBS Lett. 135, 301-303, 1981
A;Title: Human alpha-1-antitrypsin: carbohydrate attachment and sequence homology.
A;Reference number: A58526; MUID:82095611; PMID:6976274
A;Contents: annotation; carbohydrate attachment sites
C;Comment: The Z variant allele has Lys-366. Deficiency of the normal inhibitor in indiv
sis.
C;Genetics:
A;Gene: GDB:P1
A;Cross-references: GDB:120289; OMIM:107400
A;Map position: 14q32.1-14q32.1
A;Introns: 216/1; 306/2; 355/3
A;Note: the first intron occurs before the initiator codon
C;Function:
A;Description: inhibitor of serine proteinases, primarily leukocyte elastase and collage
A;Note: it also inhibits plasmin, thrombin, kallikrein, trypsin, and chymotrypsin
C;Superfamily: Serpin
C;Keywords: acute phase; emphysema; glycoprotein; plasma; polymorphism; serine proteinase
F.1-24/Domain: signal sequence #status predicted <SIG>
F.25-418/Product: alpha-1-antitrypsin #status experimental <WAT>
F.70.107.271/Binding site: carbohydrate (Asn) (covalent) #status experimental
F.382/Inhibitory site: Met (elastase, collagenase) #status experimental
Query Match 20.0%; Score 427; DB 1; Length 418;
Best Local Similarity 28.2%; Pred. No. 7.3e-24; Indels 42; Gaps 13;
Matches 120; Conservative 93; Mismatches 170;
13 LLGHSSCONPASPPEGSPDPSTGALV-----EEEDFFKVPVKNLAAAVSNFGYDLY 66

QY

Db 11 LLAGLCLVPVSLAE-----DPOGDAQKXTDTHHQDHPFP-----NKITPNLAEAFASLY 62
QY 67 VRRSMSPPTNVLSPVATALSALSAGAEORTESIIRALYYDLISSPD---IKGTYKE 124
Db 63 ROLAHQSNSTNFFSPVSIATAFAMLSLGTAKADHDEILEGLNFLTPEAQIHGEGFOE 122
QY 125 LLDVTAP--QKNLSASRIIVEFKLRIKSSVAPLEKSYGTRP-RVLTGNPRDLQELN 181
Db 123 LRLTNQPSQOLITGNGFLFSEGLKLVDFLEDVKLYHSEATVNFQDTEEAQKQIN 182
QY 182 NVVQAMQMKLARSTKEIPDEISILLGVAFKQGVTKPDSRKTSLDSDFYLDEERTVRV 241
Db 183 DYVEKGTQKIVDLVKELDRDTVFALVNYIFFKQWERPFEVKDTEEDFHDVQVTVKV 242
QY 242 PWSMDPKAVLRVYGLSDLSCK-----IAQLPLTGSMSIIFPLPLKVTQNTLIEBSLT-- 294
Db 243 PMWK-----RLGMFNIQCKKLSWLLMKYLNATAIFFLPDE--GKQLHLENELTHD 294
QY 295 --SEFTHIDRELKTVQAVLTVPKLSYEGSVTKSLQEMKLSLF-DSPDPSKITGK-P 350
Db 295 IITKPLENEDRR---SASLHLPKLSITGTVDLKSVLGQGITKVFNSGADLSGVTEAP 350
QY 351 IKLTQVHRPAGFENWEDGAGTTPSPGLQPAHLTFPLDYHLNQPFIIVLRDITDTGALLFG 410
Db 351 LKLSKAVHKAVLTIDEKGTGAAGAMFLEAIPMSIPEVKFNKPFVFLMIEQNTKSPFMG 410
QY 411 KILDP 415
Db 411 KVNP 415
RESULT 11
B39088
alpha-1-antitrypsinase F precursor - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 15-Sep-2003
C;Accession: B39088
R;Suzuki, Y.; Yoshida, K.; Honda, E.; Sinohara, H.
J. Biol. Chem. 266, 928-932, 1991
A;Title: Molecular cloning and sequence analysis of cDNAs coding for guinea pig alpha-1
A;Reference number: A39088; MUID:91093294; PMID:1985973
A;Accession: B39088
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-388 <SUZ>
A;Cross-references: GB:M38572
C;Superfamily: Serpin
Query Match 19.8%; Score 421.5; DB 2; Length 388;
Best Local Similarity 28.5%; Pred. No. 1.7e-23;
Matches 111; Conservative 88; Mismatches 155; Indels 35; Gaps 10;
QY 39 LVEEEDFPFKVPVKNLAAAVSNFGYDLYRVRSMSPPTNVLSPVATALSALSAGAQ 98
Db 20 IMAEADAQVAGPSQQIPRSLAHFAHSMYRVLITQSQNTSNITFFSPVSIATAMVSLGAKG 79
QY 99 RIESIIRALYDLYL--ISSPDINGTYKELDVTAP--QKNLSASRIIVEFKLRIKSS 154
Db 80 DTHQTILWGLEFNLTEIADIDHGFQNLHLTLNRPHSHELTGTGFLFDQNLKUKKF 139
QY 155 VAPLEKSYGTRPRVLV--GNPRDLQELNNVQAKMKLARSTKEIPDEISILLGVAHF 213
Db 140 SEDVKTYLHAEAPTTFNFSNPKAEKQINAYVEKGTQKIVDLVKLSADTLVALVNYIFF 199
QY 214 KGQVTKFDSRKTSLDSDFYLDEERTVRVPMMSDPKAVLRVYGLSDLSCKIAQ-----LPL 268
Db 200 RKGWEKPFYKHTTQEDFLVDMNTTVNVPWK-----RQGMKAFHCSTIOSWLLDY 253
QY 269 TGSMSIIFPLKVTQNTLIEBSLTSEFIHIDRELKTVQAVLTVPKLSYEGSVTKS 328
Db 254 EGNVTILFLPDK--GKMQHLEETLTPELIFKFAKTERKFNANVHLPKLSISGTVDLKEV 311

QY 329 LQEMKLOSLFD-SPDFSKIT-GKPIKLTQVHRAGFENNEDGAGTTPSPGQPAHLTFPL 386
 Db 312 LHLGITVNFSGADLSGITDMFLKIT-----BAAGATE-----LEITPHSVPO 356
 QY 387 DYHLNQPFIFVLRRDPTDTCALLFPGKILDP 415
 Db 357 DLFENKPFLLIHDSTDTPLFVGKWDMP 385

RESULT 12
 JX0129
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 15-Sep-2003
 C:Accession: JX0129; A38826; B25420; S15905; S23673; S31367
 R:Suzuki, Y.; Yamamoto, K.; Sinohara, H.
 J. Biochem. 108, 344-346, 1990
 A:Title: Molecular cloning and sequence analysis of full-length cDNA coding for mouse c
 A:Reference number: JX0129; MUID:91115777; PMID:2277027
 A:Accession: JX0129
 A:Molecule type: DNA
 A:Residues: 1-418 <SUZ>
 A:Cross-references: GB:D00725; NID:g220387; PIDN:BAA00627.1; PID:g220388
 A:Accession: A38826
 A:Molecule type: protein
 A:Residues: 30-48 <SUZ>
 R:Hill, R.E.; Shaw, P.H.; Boyd, P.A.; Baumann, H.; Hastie, N.D.
 Nature 311, 175-177, 1984
 A:Title: Plasma protease inhibitors in mouse and man: divergence within the reactive cen
 A:Reference number: A93340; MUID:84295637; PMID:6547997
 A:Accession: B25420
 A:Molecule type: mRNA
 A:Residues: 'V', 205-346, 'T', 348-418 <HIL>
 R:Ohkubo, K.; Ogata, S.; Misuma, Y.; Takami, N.; Sinohara, H.; Ikehara, Y.
 Biochem. J. 276, 337-342, 1991
 A:Title: Cloning, structure and expression of cDNA for mouse contraspin and a related p
 A:Reference number: S15905; MUID:91264784; PMID:2049065
 A:Accession: S15905
 A:Molecule type: mRNA
 A:Residues: 1-83, 'R', 85-418 <OHK>
 A:Cross-references: EMBL:X55147; NID:g50441; PIDN:CAA38948.1; PID:g50442
 A:Accession: S23673
 A:Molecule type: protein
 A:Residues: 22-41, 67-83, 156-176, 218-227, 'X', 229-235; 315-334 <OGN>
 R:Yoshida, K.; Suzuki, Y.; Sinohara, H.
 submitted to the EMBL Data Library, November 1990
 A:Description: Nucleotide and deduced amino acid sequences of contraspin from C57bl/6 m
 A:Reference number: S31367
 A:Accession: S31367
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-67, 'Q', 69, 'K', 71-192, 'K', 194-199, 'DG', 202-249, 'A', 251-303, 'S', 305-319, 'D',
 A:Cross-references: EMBL:X56786; NID:g54172; PIDN:CAA40106.1; PID:g54173
 C:Comment: Contraspin is a plasma glycoprotein.
 C:Superfamily: Serpin
 C:Keywords: Glycoprotein; serine proteinase inhibitor
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-29/Domain: propeptide #status predicted <PRO>
 F:30-418/Product: contraspin #status experimental <MAT>
 F:39,105,185,270/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.7%; Score 420; DB 2; Length 418;
 Best Local Similarity 30.9%; Pred. No. 2.4e-23;
 Matches 118; Conservative 80; Mismatches 154; Indels 30; Gaps 12;

QY 54 LAAAVSNFGDYLVRRSSMPTTNVLLSPVATALSALSGAQRTEIIHRLYYDLI 113
 Db 48 LASVNTDFAFSLYKXKALNPDNIVFSPVLSAALVSLGAKGTMEILEGLKFNLT 107
 QY 114 SSP--DIHGTYKELDDTVTAP--QKNLKSASRIVFEKLRKSSFVAPLEKSVGTRPVL 169
 Db 108 ETEADHQFGNQLSLSQEPDQDQINGNAMFIEKDQILAEF---HEK---TFLYQ 161

QY 170 TGNPRLDQEQ-----INNWTQACMKGLARSTKEIPDEISILLGVAFKQGWTKFD 222
 Db 162 TFAPTADFOQPTAKNLINDYVSNQTOGMIKELISELDELTMLVNVYIYFKRWKISFD 221
 QY 223 SRKTSLEDFYLDERTVRVPMNSDPKAVLRGLDSDLSCKIAQLPLTGSMSIIFPLPLK 282
 Db 222 PQDTFSEFYLDKRSVKVPMKMLLTTRHPRDEELSCSVLELKYTGNCASALLLPDQ- 280
 QY 283 TONLTLIEESLTSFIIHDRELKTVQ-AVLTVPKLKSVEGEVTKS-LQEMKLOSLF-D 339
 Db 281 -CRMQOVSASLQPETLRKWRKTLFPSQIEELNLPKFSIASNYRLEEDVLPENGKEVTE 339
 QY 340 SPDFSKIT-GKPIKLTQVHRAGFENNEDG-----AGTTPSGLOPAHLTFPLDYLHNOFP 394
 Db 340 QADLSGITETKLSVSQVVKAVLDVAETGTEAATAATGVIGIRKAILP---AVHFRNPP 396
 QY 395 IFVLRDPTDTCALLFPGKILDP 416
 Db 397 LFVIYHTSAQSILFMKVNPK 418

RESULT 13
 S31507
 C:Species: Apodemus sylvaticus (European woodmouse)
 C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 15-Sep-2003
 C:Accession: S31507
 R:Ingilis, J.D.; Lee, M.; Hill, R.E.
 submitted to the EMBL Data Library, December 1992
 A:Reference number: S31505
 A:Accession: S31507
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-418 <ING>
 A:Cross-references: EMBL:X69833; NID:g49418; PIDN:CAA49487.1; PID:g49419
 C:Superfamily: Serpin

Query Match 19.7%; Score 419.5; DB 1; Length 418;
 Best Local Similarity 28.1%; Pred. No. 2.6e-23;
 Matches 112; Conservative 92; Mismatches 163; Indels 31; Gaps 13;

QY 38 ALVEEDPFFKVPVKNLAAVSNFGDYLVRRSSMPTTNVLLSPVATALSALSGAE 97
 Db 31 AVQEDCNGTQVDSLTASINTDFSLYKELALNPDKNIVFSPVLSAALVSLGAK 90
 QY 98 QRTESIIRHLYDYDLISPP--DIHGTYKELDTV--TAPQKNLKSASRIVFEKLRKSS 153
 Db 91 CNTLQELLEGKFNLTETPEADIHLGFRHLLHMLSQSGKEEQINIAVSMFIEKHLQILAE 150
 QY 154 FVAPLEKSVGTRPVLTCNPRLDQEQ-----INNWTQACMKGLARSTKEIPDEISIL 206
 Db 151 FOEKVRSYI--QAAFAFA---DFQDADEARKFINDYRKETQCKIQIELSLDLVERTSMV 204
 QY 207 LLGVAHFNGQWTVTFDSRKTSLEDFYLDERTVRVPMNSDPKAVLRGLDSDLSCKIAQL 266
 Db 205 LVNVIYFKGKMKPDPDRVTLKSEFYLDKRSVKVPMKMLIEDLTPYFRDEELSCSVLEL 264
 QY 267 PLTGSMSIIFPLPKVTQNLTIEESLTSFIIHDRELKTVQ-AVLTVPKLKSVEGEV 325
 Db 265 KYIGNASALFLPDQ--GRIEQVEASLQPETLRKWKDSLPRKIDLLYLPKFLVSTDYSL 322
 QY 326 TKSLQEMKLOSLFDS-PDFSKITG-KPIKLTQVHRAGFENNEDGAGTTPSGLOPAHLT 383
 Db 323 EDVLSELGIRKSVFAQADLSRVITGKLSVSQVVKAVLEVAEKGTAAATGVK---FV 379
 QY 384 F-----PLDYHLNQPFIFVLRRDPTDTCALLFPGKILDP 415
 Db 380 FRSGRVPTMTVRFRPRPFLVTVSVGTVESILFLAKVTNP 417

RESULT 14

TTEA
 alpha-1-antitrypsin precursor - baboon (fragment)

N;Alternate names: alpha-1-proteinase inhibitor

C;Species: Papio sp. (baboon)

C;Date: 02-Apr-1992 #sequence_revision 02-Apr-1982 #text_change 15-Sep-2003

C;Accession: A01248

R;Kurachi, K.; Chandra, T.; Degen, S.J.F.; White, T.T.; Marchioro, T.L.; Woo, S.L.C.; Da

Proc. Natl. Acad. Sci. U.S.A. 78, 6826-6830, 1981

A;Title: Cloning and sequence of cDNA coding for alpha-1-antitrypsin.

A;Reference number: A01248; MUID:82082539; PMID:7031661

A;Accession: A01248

A;Molecule type: mRNA

A;Residues: 1-409 <KUR>

A;Cross-references: GB:J00321; NID:G176561; PIDN:AAA3377.1; PID:G176562

C;Comment: Alpha-1-antitrypsin is an inhibitor of serine proteinases. Its primary targeted

psin.

C;Superfamily: Serpin

C;Keywords: acute phase; glycoprotein; plasma; serine proteinase inhibitor

F;1-15/Domain: signal sequence (fragment) #status predicted <SIG>

F;16-409/Product: alpha-1-antitrypsin #status predicted <MAT>

F;61,98,262/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;373/Inhibitory site: Met (elastase, collagenase) #status predicted

Query Match 19.6%; Score 418; DB 1; Length 409;

Best Local Similarity 28.1%; Pred. No. 3.3e-23;

Matches 117; Conservative 87; Mismatches 187; Indels 26; Gaps 10;

13 LLGHSSQNPASPEEGSPDSTGALVEEDPFFK--VPVNKLAASVNFYDLYRVS 70

2 LLAGLCCLFQSLAE----DPQDAQAQKDTTPHDQNHPLINKITPSLAFAFSLYRQLA 57

71 SMSPTTNVLSPLSAVALSALSAGAQRTESIHRALYDLSPPD--IHGYKELLDT 128

58 HQSNSTNIFPSPVSIATAFAMLSLGTADTHSEILEGNFLNLTPEAQAHEGFQELLRT 117

129 VTAP--QKNLKSASRIPEKLRIRIKSSFPVAPLEKSYGTRP-RVLTGNPRLDQENNVQ 185

118 LNKSPDSQLQITGNGLFLNKLKVDKFLVDFVKNLYHSEAFNPFTEAKQINNYE 177

186 AQMGKGLARSTKEIPDEISILLGVAFKQGVTKFDSRKTSLDEFDYLDERTVRVPMMS 245

178 KGTQGVVDLVKELDRDTPFALVNYIFPKGKWRPFVEATEEEDFHDQATTVKVPMMR 237

246 DPKAVLRGLSDLSCK-----IAQLPLTGSMSIIFPLKVTQNLTLIEESLTSEIHD 300

238 -----RUGMFINVHCEKLSWMLMKYLGNATAIFFLPDE--GKLOHLENELTHDITK 289

301 IDRELKTVQAVLTVPKLSVEGVTKSLQMKLQSLF--DSPDFSKIT--GKPIKLTQVEH 358

290 FLENENRRSANLHLPKLAITGYDLKTVLGHGKITVPSNGADLSGVTEADAPLKSXAVH 349

359 PAGFPWNEDGATTPSPGLQPAHLTFPLDYHLNPPFIPLVLRDTPGALLFIGKILDP 415

350 KAVLTIDEKGTGAAGAFLEAIPMSIPPEVKFNKPFVFLMTEQNTKSPFLFGKYVNP 406

RESULT 15

S23675

N;Alternate names: related protein MC-7 precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 15-Sep-2003

C;Accession: S23675; S31506; S15632; S19078; S21870

R;Ohkubo, K.; Ogata, S.; Misumi, Y.; Takami, N.; Sinohara, H.; Ikehara, Y.

Biochem. J. 276, 337-342, 1991

A;Title: Cloning, structure and expression of cDNA for mouse contrapain and a related pr

A;Reference number: S15905; MUID:91264784; PMID:2049065

A;Accession: S23675

A;Molecule type: mRNA

A;Residues: 1-418 <CHK>

A;Cross-references: EMBL:X55148; NID:G50443; PIDN:CAA38949.1; PID:G50444

A;Experimental source: strain BAUB/c

R;Ingilis, J.D.; Lee, M.; Hill, R.E.

submitted to the EMBL Data Library, December 1992

A;Reference number: S31505

A;Accession: S31506

A;Status: Preliminary

A;Molecule type: mRNA

A;Residues: 145-312, R', 314-418 <ING>

A;Cross-references: EMBL:X69832; NID:G54174; PIDN:CAA49486.1; PID:G54175

R;Ingilis, J.D.; Hill, R.E.

EMBO J. 10, 255-261, 1991

A;Title: The murine Spi-2 proteinase inhibitor locus: a multigene family with a hyperva

A;Reference number: S15628; MUID:91122031; PMID:1991447

A;Accession: S15632

A;Status: Preliminary

A;Molecule type: DNA

A;Residues: 355-418 <IN2>

A;Cross-references: EMBL:X56820

R;Ingilis, J.D.

submitted to the EMBL Data Library, December 1990

A;Reference number: S19078

A;Status: Preliminary

A;Molecule type: DNA

A;Residues: 355-390, L', 392-418 <IN3>

A;Cross-references: EMBL:X56820

C;Superfamily: Serpin

C;Keywords: glycoprotein

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-418/Product: contrapain #status predicted <MAT>

F;104,184,269/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.6%; Score 418; DB 2; Length 418;

Best Local Similarity 28.8%; Pred. No. 3.4e-23;

Matches 119; Conservative 75; Mismatches 165; Indels 54; Gaps 11;

27 EGSPDPDSTGALVEEDPFFKVPVNKLAASVNFYDLYRVSMSPTNVLLSLSVA 86

37 ESGTPDPSLT-----LASINTDFAFSLYKELVINKPNPKNIVFSPLSIS 79

87 TALSALSAGAQRTESIHRALYDLD--TSSPDHGTGYKELLDTVTAP--QKNLKSASRI 142

80 AALAVSLGAKNTLEEILEGCKFNLTETSEADIHQGFHLLQRLSQPEDQDQINIGNAM 139

143 VPEKKLRIKSSFPVAPLEKSYGTRPRVLTGNPRLDQE-----INNVTQAAQMKGLKARS 195

140 FIEKDLQILAEFHEKARALYQTEAFT-----ADFQKPTKAKNLINDYVSNQTQGMKEL 193

196 TKEIPDEISILLGVAFKQGVTKFDSRKTSLDEFDYLDERTVRVPMMSDPKAVLRVYL 255

194 ISELDTDTLMVLVNYIFPKGKWKISFPDQDTSEFIDKRSKSVKPMKAFILTRHPR 253

256 DSDLSCKIAQLPLTGSMSIIFPLKVTQNLTLIEESLTSEFIHDIIDRELKTVQ--AVLTV 314

254 DEELSCSVLEKTYGTNASALFILPDQ--GRMQQVEASLQPETLRKWKWSLKTRKIGELYL 311

315 PKLKSVEGVTKSLQMKLQSLFD--SPDFSKITG--KPIKLTQVEHRAQFENWEDCAGTT 372

312 PKFSISTDYNLKDILPELGIKEIFSKQADLSGTTGKLSVQSVQVHKAULDVAVETGEAA 371

373 PSPG-----LQPAHLTFPLDYHLNPPFIPLVLRDTPGALLFIGKILDP 416

372 AATGTFIFGFSRRRLQNTVQVF-----NRPFLMVISHTGVTTLFMAKVTPNK 418

Search completed: September 1, 2004, 11:18:16

Job time : 42 secs

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OM protein - protein search, using sw model

Run on: September 1, 2004, 10:59:03 ; Search time 25 seconds
(without alignments)
870.613 Million cell updates/sec

Title: US-10-619-149-1

Perfect score: 2131
Sequence: 1 MQALVLLCIGALLGHSSQ.....RDTGTCALLFIGKILDPGRP 418

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

*Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2131	100.0	418	1 PEDF_HUMAN	P36955 homo sapien
2	1861	87.3	416	1 PEDF_BOVIN	Q95121 bos taurus
3	1856.5	87.1	417	1 PEDF_MOUSE	P97298 mus musculus
4	470	22.1	492	1 A2AP_BOVIN	P28800 bos taurus
5	466.5	21.9	431	1 A2AP_MOUSE	Q61247 mus musculus
6	456.5	21.4	491	1 A2AP_HUMAN	P08697 homo sapien
7	455	21.4	410	1 COTR_CAVPO	P22323 cavia porce
8	448	21.0	405	1 A1AS_CAVPO	P22325 cavia porce
9	443	20.8	413	1 CPI3_RAT	P05544 rattus norv
10	440	20.6	403	1 A1AF_CAVPO	P22324 cavia porce
11	430.5	20.2	416	1 CPI1_RAT	P05545 r contrapsi
12	429.5	20.2	413	1 ALMT_TAMSI	Q54757 tamias sibi
13	427	20.0	418	1 A1AT_HUMAN	P01009 homo sapien
14	424.5	19.9	413	1 ALMS_TAMSI	Q54758 tamias sibi
15	424.5	19.9	413	1 ALST_TAMSI	Q54760 tamias sibi
16	421.5	19.8	413	1 ALST_TAMSI	Q54759 tamias sibi
17	420	19.7	418	1 COTR_MOUSE	P07359 mus musculus
18	419.5	19.7	418	1 SI2A_APOSY	Q60396 apodemus sy
19	418	19.6	409	1 A1AT_PAPAN	P01010 papio anubi
20	415.5	19.5	406	1 CBG_SAIISC	P50451 salmisi sci
21	414	19.4	411	1 A1AT_RAT	P17475 rattus norv
22	408.5	19.2	413	1 HP55_TAMSI	Q09055 tamias sibi
23	408	19.1	413	1 A1AF_RABIT	P23035 oryctolagus
24	406.5	19.1	418	1 CPI6_RAT	P09006 rattus norv
25	405.5	19.0	413	1 A1T5_MOUSE	Q00898 mus musculus
26	404	19.0	379	1 ILEU_HORSE	P05619 equus cabal
27	403	18.9	416	1 A1AT_BOVIN	P34955 bos taurus
28	403	18.9	417	1 KBP_MOUSE	P29621 mus musculus
29	402.5	18.9	421	1 A1AT_PIG	P50447 sus scrofa
30	401.5	18.8	412	1 A1AT_CALCN	Q54763 callosciuru
31	396.5	18.6	423	1 RACT_HUMAN	P01011 homo sapien
32	395.5	18.6	500	1 ICL_HUMAN	P05155 homo sapien
33	395	18.5	405	1 CBG_HUMAN	P08185 homo sapien

34	386	18.1	416	1 A1AT_SHEEP	P12725 ovis aries
35	382	17.9	409	1 THEG_RAT	P35577 rattus norv
36	381.5	17.9	410	1 A1AT_DIDMA	Q03044 didelphis m
37	381.5	17.9	427	1 KAIN_HUMAN	P23622 homo sapien
38	380.5	17.9	413	1 A1T1_MOUSE	P07758 mus musculus
39	380.5	17.9	413	1 A1T2_MOUSE	P22599 mus musculus
40	379.5	17.8	444	1 ZPI_HUMAN	Q9UK55 homo sapien
41	379	17.8	383	1 CBG_RABIT	P23775 oryctolagus
42	378.5	17.8	378	1 ILEU_PIG	P80229 sus scrofa
43	378.5	17.8	413	1 A1T3_MOUSE	Q00896 mus musculus
44	377	17.7	430	1 CBG_SHEEP	P49920 ovis aries
45	375.5	17.6	413	1 A1T4_MOUSE	Q00897 mus musculus

ALIGNMENTS

RESULT 1
PEDF_HUMAN
ID PEDF_HUMAN STANDARD; PRT; 418 AA.
AC P36955; Q96CTI; Q96R01; Q9EWA4;
DT 01-JUN-1994 (Rel. 29, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pigment epithelium-derived factor precursor (PEDF) (EPC-1).
GN SERPINF1 OR PEDF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Eye;
RX MEDLINE=93165728; PubMed=8434014;
RA Steele F.R., Chader G.J., Johnson L.V., Tombran-Tink J.;
RT "Pigment epithelium-derived factor: neurotrophic activity and
RT identification as a member of the serine protease inhibitor gene
RT family.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:1526-1530(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Yin B., Peng X., Yuan J., Qiang B.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Wozny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schain J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 1-332 FROM N.A.
RC TISSUE=Lung fibroblast;
RA Coljee V.W.;
RL Thesis (1996), Medical College of Pennsylvania / Philadelphia, U.S.A.
RN [5]

RP SEQUENCE OF 72-418 FROM N.A.
RC TISSUE=Fibroblast;
RX MEDLINE=93232057; PubMed=8473338;
RA Pignolo R.J., Cristofalo V.J., Rotenberg M.O.;
RT "Senescent WI-38 cells fail to express EPC-1, a gene induced in young
RL cells upon entry into the G0 state.";
RN J. Biol. Chem. 268:8949-8957(1993).
[6]
RP CHARACTERIZATION.
RX MEDLINE=94043097; PubMed=8226833;
RA Becerra S.P., Palmer I., Kumar A., Steele P.R., Shiloach J.,
RT "Overexpression of fetal human pigment epithelium-derived factor in
RL Escherichia coli. A functionally active neurotrophic factor.";
RN J. Biol. Chem. 268:23148-23156(1993).
[7]
RP CHARACTERIZATION.
RX MEDLINE=96029704; PubMed=7592790;
RA Becerra S.P., Sagasti A., Spinella P., Notario V.;
RT "Pigment epithelium-derived factor behaves like a noninhibitory
RL serpin. Neurotrophic activity does not require the serpin reactive
RN loop.";
RX J. Biol. Chem. 270:25992-25999(1995).
[8]
RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS).
RX MEDLINE=21457291; PubMed=11562499;
RA Simonovic M., Gettins F.G.W., Volz K.;
RT "Crystal structure of human PEDF, a potent anti-angiogenic and neurite
RL growth-promoting factor.";
RN Proc. Natl. Acad. Sci. U.S.A. 98:11131-11135(2001).
[9]
RP VARIANT THR-72.
RX MEDLINE=9329357; PubMed=10398730;
RA Koeneke R., Pina A.L., Loyer M., Davidson J., Robitaille J.,
RT "Four polymorphic variations in the PEDF gene identified during the
RL mutation screening of patients with Leber congenital amaurosis.";
RN Mol. Vision 5:10-10(1999).
CC -1- FUNCTION: NEUROTROPHIC PROTEIN; INDUCES EXTENSIVE NEURONAL
CC DIFFERENTIATION IN RETINOBLASTOMA CELLS. POTENT INHIBITOR OF
CC ANGIOGENESIS. AS IT DOES NOT UNDERGO THE S (STRESSED) TO R
CC (RELAXED) CONFORMATIONAL TRANSITION CHARACTERISTIC OF ACTIVE
CC SERPINS, IT EXHIBITS NO SERINE PROTEASE INHIBITORY ACTIVITY.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: RETINAL PIGMENT EPITHELIAL CELLS.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN QUIESCENT CELLS.
CC -1- DOMAIN: THE N-TERMINAL (AA 44-121) EXHIBITS NEURITE OUTGROWTH-
CC INDUCING ACTIVITY. THE C-TERMINAL EXPOSED LOOP (AA 382-418)
CC IS ESSENTIAL FOR SERPIN ACTIVITY.
CC -1- SIMILARITY: Belongs to the serpin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M76979; AAA60058.1; -;
DR EMBL; AF400442; AAX92491.1; -;
DR EMBL; BC000522; AHC00522.1; -;
DR EMBL; BC013984; AAH13984.1; -;
DR EMBL; U57450; AAB38685.1; -;
DR EMBL; U57445; AAB38685.1; JOINED.
DR EMBL; U57446; AAB38685.1; JOINED.
DR EMBL; U57447; AAB38685.1; JOINED.
DR EMBL; U57448; AAB38685.1; JOINED.
DR EMBL; U57449; AAB38685.1; JOINED.
DR EMBL; M90439; AAA93524.1; -;
DR PIR; A47281; A47281.
DR PDB; 1IMV; O3-OCT-01.
DR Genew; HGNC:8824; SERPINF1.

DR MIM; 172860; -;
DR GO; GO:0004867; P:serine protease inhibitor activity; TAS.
DR GO; GO:0004868; F:serpin; TAS.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0007275; P:development; TAS.
DR GO; GO:0007357; P:histogenesis and organogenesis; TAS.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Serpin; Glycoprotein; Signal; Polymorphism; 3D-structure.
FT SIGNAL 1 15
FT CHAIN 16 418
FT ACT_SITE 382 382
FT CARBOHYD 285 285
FT VARIANT 72 72
FT FTID=VAR_009126.
FT CONFLICT 97 98
FT CONFLICT 132 132
FT HELIX 45 48
FT HELIX 50 72
FT TURN 74 75
FT STRAND 78 80
FT HELIX 82 92
FT HELIX 93 95
FT HELIX 98 107
FT TURN 108 109
FT HELIX 110 112
FT HELIX 118 129
FT TURN 130 130
FT TURN 132 133
FT STRAND 136 144
FT TURN 146 147
FT HELIX 152 162
FT STRAND 167 168
FT HELIX 173 187
FT TURN 188 190
FT STRAND 205 214
FT STRAND 217 219
FT HELIX 223 225
FT STRAND 227 232
FT STRAND 238 256
FT TURN 257 260
FT STRAND 261 268
FT TURN 269 271
FT STRAND 272 279
FT HELIX 287 290
FT TURN 291 292
FT HELIX 295 304
FT STRAND 306 315
FT STRAND 317 324
FT HELIX 326 330
FT TURN 331 335
FT HELIX 336 339
FT TURN 344 346
FT STRAND 353 364
FT STRAND 368 370
FT STRAND 387 389
FT STRAND 394 400
FT TURN 401 403
FT STRAND 406 412
FT TURN 415 416
SQ SEQUENCE 418 AA; 46342 MW; 29B573A62EA51BE5 CRC64;
Query Match 100.0%; Score 2131; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 1.5e-148;
Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQALVLLCTGALLCHSSCONPASPEEGSPDPDSTGALVEEDPFKVPNKLAASVN 60
DB 1 MQALVLLCTGALLCHSSCONPASPEEGSPDPDSTGALVEEDPFKVPNKLAASVN 60
QY 61 FGDLVVRSSMPTTNVLLSPVATLSALSLGAEQRTESIHRALYYDLSPPDING 120

Db 61 FGVDLYRVRSSMPTNNVLLSPLSVATLSALSGAEQRTESIHRALYDLSIPDHG 120
Qy 121 TYKELDTVTAPQNKLSASRIIVFEKKLRKKSFFVAPLEKSYGTRPRVTGNPRDLQEI 180
Db 121 TYKELDTVTAPQNKLSASRIIVFEKKLRKKSFFVAPLEKSYGTRPRVTGNPRDLQEI 180
Qy 181 NNWVQAMQKGLARSTKEIPDEISILLGVVAHFGQWVTKFDSRKTSLDFYLDERTYR 240
Db 181 NNWVQAMQKGLARSTKEIPDEISILLGVVAHFGQWVTKFDSRKTSLDFYLDERTYR 240
Qy 241 VPMMSDPKAVLRGLDSDLSCKIAQLPLTGSMSIIFFLPKVQNTLTIEESLTSEFIHD 300
Db 241 VPMMSDPKAVLRGLDSDLSCKIAQLPLTGSMSIIFFLPKVQNTLTIEESLTSEFIHD 300
Qy 301 IDRELKTVQAVLTPVKLKLSEYGEVTKSLQEMKLSLFDSPDPSKITGPKIKLTQVEHRA 360
Db 301 IDRELKTVQAVLTPVKLKLSEYGEVTKSLQEMKLSLFDSPDPSKITGPKIKLTQVEHRA 360
Qy 361 GFENWEDGAGTTSPGLOPAHLTFPLDYHLNQPFIFVLRDTDTGALLFGIKLDRPGP 418
Db 361 GFENWEDGAGTTSPGLOPAHLTFPLDYHLNQPFIFVLRDTDTGALLFGIKLDRPGP 418

RESULT 2

PEDF_BOVIN STANDARD; PRT; 416 AA.
ID PEDF_BOVIN STANDARD; PRT; 416 AA.
AC Q95121;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pigment epithelium-derived factor precursor (PEDF).
GN SERPINF1 OR PEDF.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RN [2]
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Retinal pigment epithelium;
RA Perez-Medavilla L., Chew C., Campochario P., Zack D.J.,
RA Becerra S.P.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Singh V.K., Chader G.J., Rodriguez I.R.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 21-47 AND 380-399.
RC TISSUE=Eye;
RX MEDLINE=96029704; PubMed=7592790;
RA Becerra S.P., Segastri A., Spinella P., Notario V.;
RT "Pigment epithelium-derived factor behaves like a noninhibitory
RT serpin. Neurotrophic activity does not require the serpin reactive
RT loop.";
RL J. Biol. Chem. 270:25992-25999 (1995).
CC -!- FUNCTION: NEUROTROPHIC PROTEIN; INDUCES EXTENSIVE NEURONAL
CC DIFFERENTIATION IN RETINOBLASTOMA CELLS. POTENT INHIBITOR OF
CC ANGIOGENESIS. AS IT DOES NOT UNDERGO THE S (STRESSED) TO R
CC (RELAXED) CONFORMATIONAL TRANSITION CHARACTERISTIC OF ACTIVE
CC SERPINS, IT EXHIBITS NO SERINE PROTEASE INHIBITORY ACTIVITY.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: RETINAL PIGMENT EPITHELIAL CELLS. LOCATED IN
CC THE INTERPHOTORECEPTOR MATRIX (IPM) WHICH IS BETWEEN THE RETINAL
CC PIGMENT EPITHELIUM AND THE NEURAL RETINA.
CC -!- DOMAIN: THE N-TERMINAL (AA 42-139) EXHIBITS NEURITE OUTGROWTH-
CC INDUCING ACTIVITY. THE C-TERMINAL EXPOSED LOOP (AA 380-416)
CC IS ESSENTIAL FOR SERPIN ACTIVITY.
CC -!- SIMILARITY: Belongs to the serpin family.
CC -----
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CC -----

DR EMBL; U48229; AAC4856.1; -.
DR EMBL; AF017059; AAC05732.1; -.
DR HSSP; P36955; INV.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Serpin; Glycoprotein; Signal.
FT SIGNAL 1 20
FT CHAIN 21 416
FT CARBOHYD 283 283
FT ACT_SITE 380 380
FT CONFLICT 21 21
FT CONFLICT 46 46
SQ SEQUENCE 416 AA; 46229 MW; F6C76B6A4C9A4ECA CRC64;

Query Match 87.3%; Score 1861; DB 1; Length 416;
Best Local Similarity 87.5%; Pred. No. 8.4e-129;
Matches 365; Conservative 23; Mismatches 27; Indels 2; Gaps 1;

Qy 1 MQALVLLICIGALGHSSCONPASPPEGSGDPDSTGALVEEDPFFKVPNKLAAAVSN 60
Db 1 MQALVLLLTGALLGFGRCQNAQ--EAGSLTPESTGAPVEEDPFFKVPNKLAAAVSN 58
Qy 61 FGVDLYRVRSSMPTNNVLLSPLSVATLSALSGAEQRTESIHRALYDLSIPDHG 120
Db 59 FGVDLYRVRSSMPTNNVLLSPLSVATLSALSGAEQRTESIHRALYDLSIPDHG 118
Qy 121 TYKELDTVTAPQNKLSASRIIVFEKKLRKKSFFVAPLEKSYGTRPRVTGNPRDLQEI 180
Db 119 TYKDLASVTAPQNKLSASRIIVFEKKLRKKSFFVAPLEKSYGTRPRVTGNPRDLQEI 178
Qy 181 NNWVQAMQKGLARSTKEIPDEISILLGVVAHFGQWVTKFDSRKTSLDFYLDERTYR 240
Db 179 NNWVQAMQKGLARSTKEIPDEISILLGVVAHFGQWVTKFDSRKTSLDFYLDERTYR 238
Qy 241 VPMMSDPKAVLRGLDSDLSCKIAQLPLTGSMSIIFFLPKVQNTLTIEESLTSEFIHD 300
Db 239 VPMMSDPKAVLRGLDSDLSCKIAQLPLTGSMSIIFFLPKVQNTLTIEESLTSEFIHD 298
Qy 301 IDRELKTVQAVLTPVKLKLSEYGEVTKSLQEMKLSLFDSPDPSKITGPKIKLTQVEHRA 360
Db 299 IDRELKTVQAVLTPVKLKLSEYGEVTKSLQEMKLSLFDSPDPSKITGPKIKLTQVEHRA 358
Qy 361 GFENWEDGAGTTSPGLOPAHLTFPLDYHLNQPFIFVLRDTDTGALLFGIKLDRPG 417
Db 359 GFENWEDGAGTTSPGLOPAHLTFPLDYHLNQPFIFVLRDTDTGALLFGIKLDRPG 415

RESULT 3

PEDF_MOUSE
ID PEDF_MOUSE STANDARD; PRT; 417 AA.
AC P97298;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pigment epithelium-derived factor precursor (PEDF) (Stromal cell-
DE derived factor 3) (SDF-3).
GN SERPINF1 OR PEDF OR SDF3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN [2]
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97092876; PubMed=8938438;
RX Shirozu M., Tada H., Tashiro K., Nakamura T., Lopez N.D., Nazarea M.,

RA Hamada T., Sato T., Nakano T., Honjo T.;
 RT "Characterization of novel secreted and membrane proteins isolated by
 RL the signal sequence trap method."; Genomics 37:273-280(1996).
 CC -!- FUNCTION: NEUTROTROPHIC PROTEIN; INDUCES EXTENSIVE NEURONAL
 CC DIFFERENTIATION IN RETINOLASTOMA CELLS. POTENT INHIBITOR OF
 CC ANGIOGENESIS. AS IT DOES NOT UNDERGO THE S (STRESSED) TO R
 CC (RELAXED) CONFORMATIONAL TRANSITION CHARACTERISTIC OF ACTIVE
 CC SERPINS, IT EXHIBITS NO SERINE PROTEASE INHIBITORY ACTIVITY (BY
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the serpin family.
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 CC -----
 CC EMBL; D50460; BAA09051.1; -;
 CC HSP; P36955; 1IMV.
 CC MGD; MG1.108080; Serpinf1.
 CC InterPro; IPR000215; Serpin.
 CC Pfam; PF00079; serpin; 1.
 CC SMART; SM00093; SERPIN; 1.
 CC PROSITE; PS00284; SERPIN; 1.
 CC Serpin; Glycoprotein; Signal.
 CC SIGNAL 1 15 POTENTIAL.
 CC CHAIN 16 417 PIGMENT EPITHELIUM-DERIVED FACTOR.
 CC ACT SITE 381 381 REACTIVE BOND (BY SIMILARITY).
 CC CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 417 AA; 46204 MW; ED680586BA74D35 CRC64;
 KW FT SIGNAL 1 15 POTENTIAL.
 KW FT CHAIN 16 417 PIGMENT EPITHELIUM-DERIVED FACTOR.
 KW FT ACT SITE 381 381 REACTIVE BOND (BY SIMILARITY).
 KW FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
 KW FT SEQUENCE 417 AA; 46204 MW; ED680586BA74D35 CRC64;
 SQ
 Query Match 87.1%; Score 1856.5; DB 1; Length 417;
 Best Local Similarity 86.5%; Pred. No. 1.8e-128;
 Matches 360; Conservative 34; Mismatches 19; Indels 3; Gaps 2;
 QY 1 MQALVLLCTGALLGHSSCON-PASPPREGSPDDSTGALVEEDPFFKVPVKNKAAAVS 59
 DB 1 MQALVLLMTGALLGHSSQNVPS--SEGPSVPDSTGEPVEEDPFFKVPVKNKAAAVS 58
 QY 60 NFGVLYRVSSSPTNNVLLSPLSVATALSALSGAEORTESIHRALYDILISPDTH 119
 DB 59 NFGVLYRLSSASPTGNVLLSPLSVATALSALSGAEHTSVIHRALYDILINPDH 118
 QY 120 GTYKELDTVTAPQKNLKSASRVFFPKLRKISSFVAPLEKSYGTRPVLTGNPRDLQ 179
 DB 119 STYKELLASVTAPEKNLKSASRVFFPKLRKISSFVAPLEKSYGTRPVLTGNPRDLQ 178
 QY 180 INNWQAQMGKLAARSTKEIPDISILLGVAFHKGQWTKFDSRKTSLDEDFVLEERTV 239
 DB 179 INNWQAQMGKLAARSTREMPSSALSILLGVAFHKGQWTKFDSRKTSLQDFHLEDRIV 238
 QY 240 RVPMSDPKAVLYGLDSDLSCKIAQLPTGSMISIFFLPKVTQNLTIIESLSEFIH 299
 DB 239 RVPMSDPKAILYGLDSDLNCKIAQLPTGSMISIFFLPVAVTQNLTIIESLSEFIH 298
 QY 300 DIDRELKTQAVLTVPKLSYGEVTKSLQENKLSQFSDPSFKITGPKLTQVEHR 359
 DB 299 DIDRELKTQAVLTVPKLSFEGELTKSQDMKLSQFSDPSFKITGPKLTQVEHR 358
 QY 360 AGPEWNEGAGTTPSPGOLPAHLTFPLDYHLNQPFFVLRTDITDGTALLFGIKILDP 415
 DB 359 AAFENWEGAGSPPSGOLQVRLTFFPLDYHLNQPFFVLRTDITDGTALLFGIKILDP 414
 RESULT 4
 A2AP BOVIN STANDARD; PRT; 492 AA.
 ID A2AP BOVIN
 AC P28800;
 DT 01-DEC-1992 (Rel. 24, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Alpha-2-antiplasmin precursor (Alpha-2-plasmin inhibitor) (Alpha-2-PI)
 DE (Alpha-2-AP).
 GN SERPINF2 OR PLI.
 OS Bos taurus (Bovine).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Euvinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94229242; PubMed=7513654;
 RA Christensen S., Berglund L., Sottrup-Jensen L.;
 RT "Primary structure of bovine alpha 2-antiplasmin."; FEBS Lett. 343:223-228(1994).
 RN [2]
 RP SEQUENCE OF 23-45 AND 374-410.
 RC TISSUE=Plasma;
 RX MEDLINE=93050153; PubMed=1385210;
 RA Christensen S., Sottrup-Jensen L.;
 RT "Bovine alpha 2-antiplasmin. N-terminal and reactive site sequence."; FEBS Lett. 312:100-104(1992).
 CC -!- FUNCTION: The major targets of this inhibitor are plasmin and trypsin, but it also inactivates chymotrypsin.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
 CC -!- SIMILARITY: Belongs to the serpin family.
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 CC -----
 CC EMBL; X78436; CA55200.1; -;
 CC PIR; S43977; S43977.
 CC HSP; P01008; IANT.
 CC InterPro; IPR000215; Serpin.
 CC Pfam; PF00079; serpin; 1.
 CC SMART; SM00093; SERPIN; 1.
 CC PROSITE; PS00284; SERPIN; 1.
 CC Acute phase; Serine protease inhibitor; Serpin; Plasma; Signal;
 KW Glycoprotein; Sulfation.
 KW SIGNAL 1 22
 FT CHAIN 23 492 ALPHA-2-ANTIPLASMIN.
 FT ACT SITE 404 405 REACTIVE BOND (FOR PLASMIN).
 FT ACT SITE 405 406 REACTIVE BOND (FOR CHYMOTRYPSIN).
 FT DISULFID 71 144 BY SIMILARITY.
 FT MOD RES 485 485 SULFATION (BY SIMILARITY).
 FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 310 310 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 317 317 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 28 28 T -> Q (IN REF. 2).
 FT CONFLICT 40 40 Q -> P (IN REF. 2).
 FT CONFLICT 43 43 Q -> E (IN REF. 2).
 SQ SEQUENCE 492 AA; 54710 MW; 075D6FC8B2DF5D CRC64;
 Query Match 22.1%; Score 470; DB 1; Length 492;
 Best Local Similarity 30.2%; Pred. No. 7e-27;
 Matches 120; Conservative 75; Mismatches 175; Indels 28; Gaps 7;
 QY 22 PASPPREG--SPDDSTGALVEEDPFFKVPVKNKAAAVSNFGVLYRVSSSPTNNVL 79
 DB 64 PKAPEDCKLSPTPEQT-----RLARAMMTFTTDLFSLVAQSSTAPNLI 108
 QY 80 LSPLSVALSALSGAEORTESIHRALYDILISPDTHGTYKELDTVTAPQKNLKS 139
 DB 109 LSPLSVALSHLALGAGNQTLQRLKEVLHAD--SGFCLPHLLSRCLQDLGPGAFRL--A 164


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SQ SEQUENCE 491 AA; 54565 MW; 385A1C90E91A63CB CRC64;
Query Match 21.4%; Score 456.5; DB 1; Length 491;
Best Local Similarity 28.1%; Pred. No. 6.7e-26;
Matches 127; Conservative 86; Mismatches 181; Indels 53; Gaps 11;

Qy 5 VLLICIGALIGHSCQNPAS-----PPEE-----GSPDPDGTAL--- 39
Dy 7 LLVLSWSCLOQPCSVFSPVAMEPLGRQLTSGPNQEQVSPULLKGNQPGQGTALKSP 66
Qy 40 --VEEDPPFKVP--VNKLAAAVSNFGVLYRVSSMSPTTNVLLSPLSVATLSALSLG 95
Dy 67 PGVCSRDP---TPQTHRLARMAWFTADLFSLVAQSTPCPNLLSPLSVALLSHLAG 123
Qy 96 AE-----QRTESIIRALYYDILSSPDHGTGTYKELLDTVTAPQPNVLSASRIPEKLR 151
Dy 124 AQNHTLQRLQVLAG-----SGPCLFHLISRLCQDLGPGAPRL--AARMYLQKGPPIK 175
Qy 152 SSFVAPLEKSYGTRPRVLTGNPRDLQELNNWQAQMKGLARSTKIPDEISTLLGVA 211
Dy 176 EDFLEQSEQLFGAKPVSLTGQEDDLANINQWKEATGKIQEFLSGLPEDTVLLLNAI 235
Qy 212 HFKQGWTKFDSRKTSLDEDFYLDERTVVRPMSPDKAVRYGLSDLSCKIAQLPTGS 271
Dy 236 HFQGFWRNKPDPSTQDSDPHLDEQFTVPVEMQARTYPLRWFLLEQPEIQVAHFPFKNN 295
Qy 272 MSITFFLPKVTQNTLIEESLSEFTHD---IDRELKTQVAVLTVPKLSYGEVTKS 328
Dy 296 MSFVVLVTHEFVWVSQVLANLWDTLHPVLWBRPTK-----VRLPKLYLKQMDLVAT 350
Qy 329 LQEMKLOSLFSPSPFKITGPVKITQVEHVRAGFENWEDGAGTTPSPGLQPAHLTFPLDY 388
Dy 351 LSQGLQELFQAPDLRGISEQSLVSGVGHQSTLELSEVGEAAATSIAMRSVLS-SF 409
Qy 389 HLNQPFVPLRDTDTGALLFGKILDP 415
Dy 410 SVNRPFLEFIEDTGLPLFVGSVRNP 436

RESULT 7
COTR_CAVPO STANDARD; PRT; 410 AA.
ID ALIAS_CAVPO STANDARD; PRT; 405 AA.
AC P22325;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alpha-1-antiprotease S precursor (Alpha-1-antitrypsin) (Alpha-1-
DE prteinase inhibitor) (AFS).
DE Cavia porcellus (Guinea pig).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 25-44.
RA MEDLINE=91093294; PubMed=1985973;
RX Suzuki Y., Yoshida K., Honda E., Sinohara H.;
RT "Molecular cloning and sequence analysis of cDNAs coding for guinea
RT pig alpha 1-antiproteases S and F and contrapsin.";
RL J. Biol. Chem. 266:928-932(1991).
CC -!- FUNCTION: CONTRAPSIN INHIBITS TRYPSIN-LIKE PROTEASES.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- SIMILARITY: Belongs to the serpin family.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M57269; AAA62806.1; --.
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DR PIR; C39088; C39088.
DR HSSP; P01009; 8API.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Serpin; Serine protease inhibitor; Plasma; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 410
FT ACT_SITE 374 375
FT CARBOHYD 62 62
FT CARBOHYD 99 99
FT CARBOHYD 162 162
FT CARBOHYD 229 229
FT CARBOHYD 263 263
SQ SEQUENCE 410 AA; 45599 MW; A5931286FA4605A0 CRC64;

Query Match 21.4%; Score 455; DB 1; Length 410;
Best Local Similarity 28.1%; Pred. No. 6.7e-26;
Matches 111; Conservative 101; Mismatches 159; Indels 24; Gaps 9;

Qy 37 GALVEE---EDPFFKVPVNKLAAAVSNFGVLYRVSSMSPTTNVLLSPLSVATLSAL 92
Dy 21 GIMAEDIQVAPSQHMPSHKVPVSLAHFAHSHRVLTQQSNTSIFPSVATIALAV 80
Qy 93 SLGAEQRTESIIRALYYDILSSPDHGTGTYKELLDTVTAP--QNKLSASRIPEKXL 148
Dy 81 SLGAKGDTHTQILRSLEFNLTAEADIDHGFQNLHLTLNRPHSEHQLTTGNGFLDQNL 140
Qy 149 RIKSSVAPLEKSYGTRPRVLT--GNPRDLQELNNWQAQMKGLARSTKIPDEISTILL 207
Dy 141 KLKEKESGVKTLYHAAEFPTNFSNPKEAKINAYVEKGTQKIVDLYKDLGADTVLAL 200
Qy 208 LGVAHFKGQWTKFDSRKTSLDEDFYLDERTVVRPMSPDKAVRYGLSDLSCKIAQ-- 265
Dy 201 VNIFPGRKWEKPFQVKTQEDFHVDAANTTVKVPNMK-----QQGMKHAHCSTIQSW 254
Qy 266 ---LPLTGSMSIIFFLPKVTQNTLIEESLSEFTHDIDRELKTQVAVLTVPKLSYGE 322
Dy 255 VLLLDYEGNVTALFLLPDE--GKMQLHELTLPFLVFKFLRKTETMPAYVLPKLSIGT 312
Qy 323 GEVTKLSQEMKLOSLFD--SPDPSKIT--GKPIKLTQVEHVRAGFENWEDGAGTTPSPGLQPA 380
Dy 313 YDLKEVLRDLGNTNVFSGAADLSGITEDNPLKSLKGLHRLTIDEGTEAAATVLEAT 372
Qy 381 HLNQPFVPLRDTDTGALLFGKILDP 415
Dy 373 RTARPRLSNKPFPELLIDHSDTDTPLFVGKVM DP 407

RESULT 8
ALIAS_CAVPO STANDARD; PRT; 405 AA.
ID ALIAS_CAVPO STANDARD; PRT; 405 AA.
AC P22325;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alpha-1-antiprotease S precursor (Alpha-1-antitrypsin) (Alpha-1-
DE prteinase inhibitor) (AFS).
DE Cavia porcellus (Guinea pig).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 25-44 AND 75-93.
RX MEDLINE=91093294; PubMed=1985973;
RX Suzuki Y., Yoshida K., Honda E., Sinohara H.;
RT "Molecular cloning and sequence analysis of cDNAs coding for guinea
RT pig alpha 1-antiproteases S and F and contrapsin.";
RL J. Biol. Chem. 266:928-932(1991).
CC -!- FUNCTION: INHIBITS ELASTASE, CHYMOTRYPSIN, CATHEPSIN G, PLASMIN,
CC AND TRYPSIN.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC
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Db 105 EITEEHQGFHLLORLSQDOVEINTGSALFIDKEQFILSEFOBKTRALYQAEAFIA 164
 QY 170 T-GNPRDLQELNNWQAKMGKLARSTKIPDEISILLGVAFKQWTKFDSKTSLS 228
 Db 165 DFKQFNBAKLLINDVSNQOGKIAELFSLDEERTSMVLNLLFKGKVKVPNPNDTFE 224
 QY 229 EDFYLDERTVRVPMMSDPRKAVLRYGLDSDLSCKIAQLPLTGSMSIIFFLPLKVTQNLTL 288
 Db 225 SEFYLDKRSVKVPMKIKETVTPYVDEELSCSVLELKYTGNASALFILPDQ--GKMQQ 282
 QY 289 IEESLTSEFHD-IDRELKTVQAVLTPVKLSYGEVETKLSQMKLQSLF-DSPDFSKI 346
 Db 283 VESSLOPETLKKWKDSDIPRIINDLRMPKFSISTDYSLKVELPGLGKVKVFSQAADLSRI 342
 QY 347 TG-KPIKLTQVEHVRAGFEMNEDGAGTTPSPQLQPAHLTFPLDYHLNQPFFVLRLDITDGA 405
 Db 343 TGYKDLVSVQVHKAVLDVDETGTATAGVATVIRQRPTLNFRPFWVITDMSQS 402
 QY 406 LLFTGKILDR 416
 Db 403 ILFAKITNPK 413

RESULT 10

AIAT_CAVPO STANDARD; PRT; 403 AA.
 AC P22324;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Alpha-1-antitrypsin F precursor (Alpha-1-antitrypsin) (Alpha-1-
 DE proteinase inhibitor) (APF) (fragment).
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 23-42 AND 73-91.
 RX MEDLINE=91093294; PubMed=1985973;
 RA Suzuki Y., Yoshida K., Honda E., Sinozara H.;
 RT "Molecular cloning and sequence analysis of cDNAs coding for guinea
 RT pig alpha 1-antitrypsinases S and F and contrapain.;
 RL J. Biol. Chem. 266:928-932(1991).
 CC -1- FUNCTION. INHIBITS ELASTASE, CHYMOTRYPSIN, CATHEPSIN G, PLASMIN,
 CC AND TRYPSIN.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- INDUCTION: APF ROSE ABOUT 2-FOLD DURING THE ACUTE PHASE REACTION.
 CC -1- SIMILARITY: Belongs to the serpin family.
 CC -----
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 CC -----
 CC EMBL; M57271; AAA62804.1; --
 DR HSSP; P01009; 9AP1.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 KW Acute phase; Serine protease inhibitor; Serpin; Plasma; Signal;
 KW Glycoprotein.
 FT NON_TER 1 1
 FT SIGNAL <1 22
 FT CHAIN 23 403
 FT ACT_SITE 367 368
 FT ACT_SITE 55 55
 FT CARBOHYD 92 92
 FT CARBOHYD 155 155
 FT CARBOHYD 222 222

FT CARBOHYD 256 256 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 403 AA; 44919 MW; C39729EB364D909B CRC64;
 Query Match 20.6%; Score 440; DB 1; Length 403;
 Best Local Similarity 28.8%; Pred. No. 8.2e-25;
 Matches 112; Conservative 92; Mismatches 165; Indels 20; Gaps 8;
 QY 39 LVEEDPPFPKVPVKNLAAVSNFGVDLYRVSSMPTTNVLLSPLSVATALSALSGAEQ 98
 Db 20 IWAEDAQVAGPSQIQPSLAFHAFSHMYRVLTQOSNTSNIFSPVSIATIALAMVSLGAKG 79
 QY 99 RTESIIRALYYDL--ISSPDHGYKELDTVTAP--QKNLKSASRIVFEKKLRKSGSF 154
 Db 80 DTHQTQLWGLEPFLNLTAEADITHDGFQNLTLNRPHESEHETLNGFLDQKLKKEKF 139
 QY 155 VAPLEKSYGTRPRVLT-GNPRDLQELNNWQAKMGKLARSTKIPDEISILLGVAFH 213
 Db 140 SEDVKTLYLHAEAPPTNFNPKAEKQINAYVEKGTQGIKIVLVDKLSADTVLALVNYIFF 199
 QY 214 KQGVTKFDSRKTSLSEDFYLDERTVRVPMMSDPRKAVLRYGLDSDLSCKIAQ----LPL 268
 Db 200 RCKWEKPFQVHTTQEDFLVDMNTTVNVPMMK-----RQGMKAFHCSSTIQSWLLLDY 253
 QY 269 TGSMSIIFPLPKVTQNLTLSESTSEFIHDIIDRELKTVQAVLTPVKLSYGEVETKS 328
 Db 254 EGNVTTLFLLPDK--GKMQHLEETLTPELIFKPARKTERMFANVHLPKLSISGTYYDLKEV 311
 QY 329 LOEMKLOSLFD-SPDFSKIT-GKPIKLTQVEHVRAGFEMNEDGAGTTPSPQLQPAHLTPPL 386
 Db 312 LGHLGITNVFSGAADLSGITEDMPLKISKGLHALLTIDKGTAEAGATELEITHSVPO 371
 QY 387 DVHLNQPIFVLRLDTDTGALLFIGKILDP 415
 Db 372 DLFFNKPFLFIIDHSTDTPLFVGKVMDP 400
 RESULT 11
 CPIL_RAT STANDARD; PRT; 416 AA.
 ID CPIL_RAT
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Contrapain-like protease inhibitor 1 precursor (CPI-21) (Kallikrein-
 DE binding protein) (KBP) (Growth hormone-regulated proteinase inhibitor)
 DE (Serine protease inhibitor 2) (SPI-2) (GHR-P63) (SPI-2.3) (Thyroid
 DE hormone-regulated protein).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RC MEDLINE=91340751; PubMed=1874745;
 RA Chai K.X., Ma J.-X., Murray S.R., Chao J., Chao L.;
 RT "Molecular cloning and analysis of the rat kallikrein-binding protein
 RT gene.;
 RL J. Biol. Chem. 266:16029-16036(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=90306038; PubMed=1694763;
 RA Pages G., Rouyrenc J.F., le Cam G., Mariller M., le Cam A.;
 RT "Molecular characterization of three rat liver serine-protease
 RT inhibitors affected by inflammation and hypophysectomy. Protein and
 RT mRNA analysis and cDNA cloning.;
 RL Eur. J. Biochem. 190:385-391(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=87166046; PubMed=3494016;
 RA Yoon J.-B., Towle H.C., Seelig S.;

RA Vaughan L., Boswell D.R.;
 RT "Structure and variation of human alpha 1-antitrypsin.";
 RL Nature 298:329-334(1982).
 RN [10]
 RP PRELIMINARY SEQUENCE OF 25-418.
 RA Chan S.K.;
 RT "The covalent structure of human alpha1-protease inhibitor.";
 RL Fed. Proc. 41:1016-1016(1982).
 RN [11]
 RP SEQUENCE OF 1-67; 196-255 AND 387-418 FROM N.A.
 RX MEDLINE=82220035; PubMed=6979715;
 RA Leicht M., Long G.L., Chandra T., Kurachi K., Kidd V.J., Mace M. Jr.,
 RA Davis E.W., Woo S.L.C.;
 RT "Sequence homology and structural comparison between the chromosomal
 RT human alpha 1-antitrypsin and chicken ovalbumin genes.";
 RL Nature 297:655-659(1982).
 RN [12]
 RP SEQUENCE OF 291-418 FROM N.A.
 RX MEDLINE=86005469; PubMed=3876243;
 RA Riley J.H., Bathurst I.C., Edbrooke M.R., Carrell R.W., Craig R.K.;
 RT "Alpha 1-antitrypsin and serum albumin mRNA accumulation in normal,
 RT acute phase and ZZ human liver.";
 RL FEBS Lett. 189:361-366(1985).
 RN [13]
 RP SEQUENCE OF 350-418 FROM N.A.
 RX MEDLINE=82082539; PubMed=7031661;
 RA Kurachi K., Chandra T., Friezen Degen S.J., White T.T.,
 RA Marchioro T.L., Woo S.L.C., Davies E.W.;
 RT "Cloning and sequence of cDNA coding for alpha 1-antitrypsin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:6826-6830(1981).
 RN [14]
 RP SEQUENCE OF 387-418 FROM N.A.
 RX MEDLINE=85225507; PubMed=3873938;
 RA Coutelle C., Speer A., Rogers J., Kalsheker N., Humphries S.,
 RA Williamson R.;
 RT "Construction and partial characterization of a human liver cDNA
 RT library.";
 RL Biomed. Biochim. Acta 44:421-431(1985).
 RN [15]
 RP CARBOHYDRATE-LINKAGE SITES ASN-70 AND ASN-271.
 RX MEDLINE=22660472; PubMed=12754519;
 RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;
 RT "Identification and quantification of N-linked glycoproteins using
 RT hydrazide chemistry, stable isotope labeling and mass spectrometry.";
 RL Nat. Biotechnol. 21:660-666(2003).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RX MEDLINE=84292309; PubMed=6332197;
 RA Loebermann H., Tokuka R., Deisenhofer J., Huber R.;
 RT "Human alpha 1-proteinase inhibitor. Crystal structure analysis of
 RT two crystal modifications, molecular model and preliminary analysis
 RT of the implications for function.";
 RL J. Mol. Biol. 177:531-556(1984).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RX MEDLINE=89221004; PubMed=2785270;
 RA Eigh R., Loebermann H., Schneider M., Wiegand G., Huber R.,
 RA Laurell C.-B.;
 RT "The s variant of human alpha 1-antitrypsin, structure and
 RT implications for function and metabolism.";
 RL Protein Eng. 2:407-415(1989).
 RN [18]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=20386623; PubMed=10933492;
 RA Elliott P.R., Fei X.Y., Dafforn T.R., Lomas D.A.;
 RT "Topography of a 2.0 A structure of alpha1-antitrypsin reveals targets
 RT for rational drug design to prevent conformational disease.";
 RL Protein Sci. 9:1274-1281(2000).
 RN [19]
 RP REVIEW.
 RX MEDLINE=89352843; PubMed=2669992;
 RA Kalsheker N.;
 RT "Alpha 1-antitrypsin: structure, function and molecular biology of

RT the gene.";
 RL Biosci. Rep. 9:129-138(1989).
 RN [20]
 RP REVIEW.
 RX MEDLINE=91315455; PubMed=1859394;
 RA Wu Y., Foreman R.C.;
 RT "The molecular genetics of alpha 1 antitrypsin deficiency.";
 RL Bioessays 13:163-169(1991).
 RN [21]
 RP DESCRIPTION OF VARIANT M2.
 RX MEDLINE=89324438; PubMed=2901226;
 RA Nukiwa T., Brantly M.L., Ogushi F., Fells G.A., Crystal R.G.;
 RT "Characterization of the gene and protein of the common alpha 1-
 RT antitrypsin normal M2 allele.";
 RL Am. J. Hum. Genet. 43:322-330(1988).
 RN [22]
 RP VARIANT M3 ASP-400.
 RX MEDLINE=90368097; PubMed=2394452;
 RA Graham A., Hayes K., Weidinger S., Newton C.R., Markham A.F.,
 RA Kalsheker N.A.;
 RT "Characterisation of the alpha-1-antitrypsin M3 gene, a normal
 RT variant.";
 RL Hum. Genet. 85:381-382(1990).
 RN [23]
 RP VARIANT F CYS-247.
 RX MEDLINE=91241132; PubMed=2035534;
 RA Okayama H., Brantly M., Holmes M., Crystal R.G.;
 RT "Characterization of the molecular basis of the alpha 1-antitrypsin F
 RT allele.";
 RL Am. J. Hum. Genet. 48:1154-1158(1991).
 RN [24]
 RP VARIANT M-HEERLEN LEU-393.
 RX MEDLINE=89154435; PubMed=2784123;
 RA Hofker M.H., Nukiwa T., van Paassen H.M.B., Nelen M., Kramps J.A.,
 RA Klaasen E.C., Frants R.R., Crystal R.G.;
 RT "A Pro->Leu substitution in codon 369 of the alpha-1-antitrypsin
 RT deficiency variant PI M-Heerlen.";
 RN [25]
 RP Query Match 20.0%; Score 427; DB 1; Length 418;
 RP Best Local Similarity 28.2%; Pred. No. 7.8e-24;
 RP Matches 120; Conservative 93; Mismatches 170; Indels 42; Gaps 13;
 QY 13 LLGHSSQNPASPPPEEGSPDSTGALV-----EEDPEFKVPVVKLAASVNFVGLY 66
 DB 11 LLAGLCLVPVSLAE-----DPQDAQKTDTSHHQDHPF-----NKITNLAEFAFSLY 62
 QY 67 RVRSMSPTTNVLSPLSVATALSALSGAEQRTESIHRALYDYLSSPD--IHGTKE 124
 DB 63 RLALHQSNTNIPSPVSIATAFAMLSLGTADTHDEILEGLNFLTIEPAQIHGEFQE 122
 QY 125 LLDVTWAP--QKNLKSASRIVFEKLIKSSVAPLEKSYGTRP-RVLTGNPLDLQEQIN 181
 DB 123 LLRTINQPSQLQLTTCNGFLFSEGLKLVDFKLEVDKGLYHSEAFVNFQDTEAKKQIN 182
 QY 182 NWQAMQMGKLARSTKIPDEISTLLIGVAHFQGWTKFDSRKTSLDEFLDEERTVY 241
 DB 183 DYVEKGTQGLVDLVKELDRDTVFALVNYIFFKQWPERPEVKDTEEDFHVQVTVKV 242
 QY 242 PMSDPKAVRYGLDSDLSCK-----IAQLPLTGSMSIIFFLPKVTQNTLIESLT-- 294
 DB 243 PMK-----RLGMFTQHKCKLSSWVLLMKYLNATAIFFLPDE--GKLQHLNELTHD 294
 QY 295 --SEFIHDIDRELKTVQAVLTVPKLLSYEGEVTKSLQEMKLSLF--DSPDFSKITGK-P 350
 DB 295 IITFLENERD-----SASHLPKLSITGYDLSKVLGQLGITKVSNGADLSGVTEEP 350
 QY 351 IKLQVQEHRAQFENEDAGTTPSPGLQPAHLFFPDYHNLNQPFIVFLRDTDTGALLFIG 410
 DB 351 LKLSKAVHKAULTIDKRGTEAAGAMFLEAFPMISIPPEVKFNKPFVFLMTBQNTKSPFMG 410
 QY 411 KILDP 415
 DB 411 KVNVP 415

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RESULT 14
ALMS_TAMSI
ID ALMS_TAMSI STANDARD; PRT; 413 AA.
AC OS4758;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-1-antitrypsin-like protein CM55-MS precursor.
OS Tamas sibiricus (Siberian chipmunk) (Asian chipmunk).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
OC Tamias.
CX NCBI_TaxID=64680;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98094263; PubMed=94341474;
RA Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,
RA Tsutou S., Watanabe M., Kondo J., Kondo N., Shiba T.;
RA "Expression of multiple alphas-1-antitrypsin-like genes in hibernating
RT species of the squirrel family."
RL Gene 204:127-132(1997).
CC -!- TISSUE SPECIFICITY: Expressed in liver.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. HIGH, TO ALPHA-1-
CC ANITRYPSIN.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB000547; BAA24417.1; -.
CC HSP; P01009; IQLP.
CC InterPro; IPR000215; Serpin.
CC Pfam; PF00079; serpin; 1.
CC SMART; SM00093; SERPIN; 1.
CC PROSITE; PS00284; SERPIN; 1.
CC Serpin; Serine protease inhibitor; Glycoprotein; Signal;
CC Pyroglutamate carboxylic acid.
CC SIGNAL 1 24 POTENTIAL.
CC CHAIN 25 413 ALPHA-1-ANTITRYPSIN-LIKE PROTEIN CM55-MS.
CC MOD_RES 25 25 PYROGLUTAMATE CARBOXYLIC ACID (POTENTIAL).
CC FT CARBOHYD 65 65 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 102 102 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 266 266 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT ACT_SITE 377 378 REACTIVE BOND (BY SIMILARITY).
CC SQ SEQUENCE 413 AA; 45952 MW; 430374CA26EBAF08 CRC64;

Query Match
Best Local Similarity 28.2%; Score 424.5; DB 1; Length 413;
Matches 119; Conservative 101; Mismatches 169; Indels 33; Gaps 14;

QY 7 LLCIGALLGHSQCNAPSPPEEGSDSTGALVEEDPFPKVPVKNLAASVNFYDLY 66
Db 9 LLLLAAL----SLGPGSLAQDAQ---ETEASQDQEH-----ASHRIAPHLAEFALSLY 57
QY 67 RVSSMPTTNVLLSPSLVATASLSLGAQETSTIHRALYDYL--TSSPDHGTKE 124
Db 58 RVLRQNTNTNIFSPVSIATAMLSLGTGKGDTHQILEGLDFNTEMAEDIHGQFOR 117
QY 125 LLDVTWAP--QXNLSASRIVFEKKRIKSSFVAPLEKSYGTG--PRVLTGNPRDLQRI 180
Db 118 LLQTLNRPNTQLQTSNGLFHQNKLKLDKFLVDKLSYHSEAFNTFT--NWEERARQOI 176
QY 181 NNWVQAMQKGLARSTKEIPDEISILLGVHFKGQWTKFDSRKTSLSDFYLDERTVR 240
Db 177 NSYVEKGTQKGLVELKELSDTVALVNVYFFKGLKLPFPNEHTREEDFHVDEATTVR 236

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QY 241 VPMSPDKAVLRIGLD--SDLSCKIAQLPLTSMGSIIFLPLKVTQNLTLIESITSEPI 298
Db 237 VPMNREG---RFHLHCSTLASVQLMDYLNATAIFLLPDE--GKQOHLSDTSTETIL 291
QY 299 HOIDRELKTVQAVLTPVKLSYEGETVSKLQEMKLSLF-DSPDFSKITGK-PKLTGV 356
Db 292 SKFLNKRQTRVSLYFPKVSIGTVALKTVLSSIGITKVFNSAADLSGVTEAPLIVSKA 351
QY 357 EHRAGFENNEDGAGTTPSPGLOPAHLTF---PLDYHLNQPFVFLVRLDTHDGTGALLFGIKL 413
Db 352 LHKAVLIDDEG---TEAAGATVGGTFTWSPRKEVIFDRPFLVVIYEHHTKSPLEFGKV 408
QY 414 DP 415
Db 409 NP 410

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RESULT 15
ALSI_TAMSI
ID ALSI_TAMSI STANDARD; PRT; 413 AA.
AC OS4760;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-1-antitrypsin-like protein CM55-SI precursor.
OS Tamas sibiricus (Siberian chipmunk) (Asian chipmunk).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
OC Tamias.
CX NCBI_TaxID=64680;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98094263; PubMed=94341474;
RA Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,
RA Tsutou S., Watanabe M., Kondo J., Kondo N., Shiba T.;
RA "Expression of multiple alphas-1-antitrypsin-like genes in hibernating
RT species of the squirrel family."
RL Gene 204:127-132(1997).
CC -!- TISSUE SPECIFICITY: Expressed in liver.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. HIGH, TO ALPHA-1-
CC ANITRYPSIN.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB000549; BAA24419.1; -.
CC HSP; P01009; 9API.
CC InterPro; IPR000215; Serpin.
CC Pfam; PF00079; serpin; 1.
CC SMART; SM00093; SERPIN; 1.
CC PROSITE; PS00284; SERPIN; 1.
CC Serpin; Serine protease inhibitor; Glycoprotein; Signal;
CC Pyroglutamate carboxylic acid.
CC SIGNAL 1 24 POTENTIAL.
CC CHAIN 25 413 ALPHA-1-ANTITRYPSIN-LIKE PROTEIN CM55-SI.
CC MOD_RES 25 25 PYROGLUTAMATE CARBOXYLIC ACID (POTENTIAL).
CC FT CARBOHYD 65 65 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 102 102 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 266 266 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT ACT_SITE 377 378 REACTIVE BOND (BY SIMILARITY).
CC SQ SEQUENCE 413 AA; 46202 MW; AB65AID31B8CA2EC CRC64;

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Query Match
Best Local Similarity 19.9%; Score 424.5; DB 1; Length 413;
Matches 119; Conservative 100; Mismatches 169; Indels 35; Gaps 13;

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QY	7	LICI	GALLGHSC	QNCPAS	PPPEEGSP	DPDSTG	ALVEED	PFKVPV	KNKLA	AAVSNF	GDIY	66
		::	::	::	::	::	::	::	::	::	::	
Db	9	LLLL	LAAL	----	SC	PGSLAQ	DAQ	----	ET	BASKQDQ	HP	57
		::	::	::	::	::	::	::	::	::	::	
QY	67	RYR	SMSP	PTNV	LLSP	LS	AVAT	AL	SAL	SALG	AEQRT	124
		::	::	::	::	::	::	::	::	::	::	
Db	58	RV	LARQ	SNT	TH	FF	SP	VS	IAT	AL	ML	117
		::	::	::	::	::	::	::	::	::	::	
QY	125	L	D	T	V	T	A	P	-	Q	N	181
		::	::	::	::	::	::	::	::	::	::	
Db	118	L	I	Q	T	N	R	E	N	T	Q	177
		::	::	::	::	::	::	::	::	::	::	
QY	182	N	V	Q	A	M	G	K	L	A	R	241
		::	::	::	::	::	::	::	::	::	::	
Db	178	S	V	E	G	T	G	K	V	I	L	237
		::	::	::	::	::	::	::	::	::	::	
QY	242	P	M	S	D	F	K	A	V	L	R	296
		::	::	::	::	::	::	::	::	::	::	
Db	238	P	M	N	-	----	R	G	M	P	H	289
		::	::	::	::	::	::	::	::	::	::	
QY	297	F	H	I	D	R	E	L	K	T	V	354
		::	::	::	::	::	::	::	::	::	::	
Db	290	I	L	T	K	L	K	N	E	T	T	349
		::	::	::	::	::	::	::	::	::	::	
QY	355	Q	V	E	R	A	G	F	E	N	D	412
		::	::	::	::	::	::	::	::	::	::	
Db	350	K	A	L	H	A	V	I	D	E	-	407
		::	::	::	::	::	::	::	::	::	::	
QY	413	L	D	P	415							
		::	::									
Db	408	V	N	P	410							
		::	::									

Search completed: September 1, 2004, 11:15:27
Job time : 28 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2004, 11:07:34 ; Search time 119 Seconds
(without alignments)
1108.291 Million cell updates/sec

Title: US-10-619-149-1
Perfect score: 2131
Sequence: 1 MQALVLLLCIGALLGHSSCQ.....RDTGALLFGIKILDRGP 418

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriaph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1856.5	87.1	417	11	O70629
2	1851.5	86.9	417	11	O88691
3	1788	83.9	418	11	O802A3
4	1784	83.7	362	4	Q13236
5	537	25.2	448	13	O42453
6	456.5	21.4	491	4	Q8N5U7
7	453	21.3	471	11	Q80X76
8	441.5	20.7	420	11	Q60552
9	429.5	20.2	415	6	Q9GMA6
10	421	19.8	418	11	Q8VCH3
11	420	19.7	418	11	Q91X80
12	418	19.6	418	11	Q03734
13	418	19.6	423	11	P97569
14	417	19.6	406	11	Q64118
15	416.5	19.5	418	11	Q91WP6
16	416.5	19.5	418	11	Q62258

17	416	19.5	418	11	Q91W80
18	413	19.4	412	11	Q63556
19	411.5	19.3	396	6	O00394
20	406.5	19.1	411	6	Q9TTE1
21	403	18.9	413	6	Q07298
22	402	18.9	413	11	Q7TME5
23	400	18.8	375	11	O8K3Y1
24	400	18.8	418	11	Q62257
25	399	18.7	413	11	Q9CQ32
26	396	18.6	413	6	Q28665
27	395.5	18.6	423	11	Q63969
28	395.5	18.6	423	4	O8N177
29	393.5	18.5	432	13	O7SYX0
30	392.5	18.4	500	4	O96PE0
31	392	18.4	405	4	Q722Q9
32	391.5	18.4	421	6	O46519
33	390.5	18.3	413	11	O54761
34	390.5	18.3	440	4	Q86U17
35	387	18.2	456	6	O62663
36	385.5	18.1	407	4	Q9UNU9
37	384	18.0	413	6	Q28666
38	383.5	18.0	413	11	O54762
39	382	17.9	379	11	Q9D154
40	381.5	17.9	413	11	Q91XB8
41	381.5	17.9	413	11	Q8VC20
42	381.5	17.9	422	11	Q80YB8
43	381.5	17.9	425	11	O80ZHS
44	381.5	17.9	436	11	O8ZV6
45	381	17.9	418	11	Q9D7D2

ALIGNMENTS

RESULT 1
O70629
ID O70629 PRELIMINARY; PRT; 417 AA.
AC O70629;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Pigment epithelium-derived factor (Serine (or cysteine) proteinase
DE inhibitor, clade F (Alpha-2 antip-amin, pigment epithelium derived
DE factor). member 1)).
GN SERPINF1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Singh V.K., Chader G.J., Rodriguez I.R.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; AF017055; AAC05733.1; -.
DR EMBL; AF017051; AAC05733.1; JOINED.
DR EMBL; AF017052; AAC05733.1; JOINED.
DR EMBL; AF017053; AAC05733.1; JOINED.
DR EMBL; AF017054; AAC05733.1; JOINED.
DR EMBL; AF017057; AAC05731.1; -.
DR EMBL; BC019852; AAH19852.1; -.
DR HSSP; P36955; 1IMV.
DR MGD; MGI:108080; Serpinf1.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.

KW Protease inhibitor; Serine protease inhibitor; Serpin.
SQ SEQUENCE 417 AA; 46234 MW; ECD360FE6AA74D25 CRC64;

Query Match 87.1%; Score 1856.5; DB 11; Length 417;
Best Local Similarity 86.5%; Pred. No. 1.6e-136;
Matches 360; Conservative 34; Mismatches 19; Indels 3; Gaps 2;

QY 1 MQALVLLICIGALLGHSSCON--PASPPPEGSDPDSTGALVEBEDPFFKVPVKNKLAASV 59
DB 1 MQALVLLICIGALLGHSSCON--SEGSPVDPSTGEPVEBEDPFFKVPVKNKLAASV 58

QY 60 NFGYDLVVRSSMPTTNVLLSPLSVATALSALSGAEQRTESIIRALYYDLITSPDIH 119
DB 59 NFGYDLVRLSSASPTGNVLLSPLSVATALSALSGAEHRTESIIRALYYDLITNPDIH 118

QY 120 GTYKELDTVTAPQKNLKSASRIIVFEKLRKKSFPVAPLEKSYGTRPRVLTGNPRDLQ 179
DB 119 STYKELLASVTAPKKNLKSASRIIVFEKLRKKSFPVAPLEKSYGTRPRILTGNPRVDLQ 178

QY 180 INNVOQOMKGLARSTKEIPDEISILLGVAFKQGWTKFDSRKTSLDFVLDERTV 239
DB 179 INNVOQOMKGLARSTKEIPDEISILLGVAFKQGWTKFDSRKTSLDFVLDERTV 238

QY 240 RVPWMSDPKAVIRYGLSDLSCKIAQLPLTGSMIIFFPLKVTQNTLTIEESLTSEFIH 299
DB 239 RVPWMSDPKAVIRYGLSDLSCKIAQLPLTGSMIIFFPLKVTQNTLTIEESLTSEFIH 298

QY 300 DIDRELKTQAVLTVPKLSYEGEVTKSLQEMKLSQSLFSDPFSKTKGPKLTQVEHR 359
DB 299 DIDRELKTQAVLTVPKLSYEGEVTKSLQEMKLSQSLFSDPFSKTKGPKLTQVEHR 358

QY 360 AGFENWEDGAGTTSPGLQPAHLTFPLDYHLNQPFIFVLRDRTDTGALLFGKILDP 415
DB 359 AAFENWEGAGSSPGLQPVRLTFPLDYHLNQPFIFVLRDRTDTGALLFGKILDP 414

RESULT 3
Q80ZA3 PRELIMINARY; PRT; 418 AA.
ID Q80ZA3
AC Q80ZA3
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-2 antipain.
GN DMRS91.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RA Yang J.L., Yang Y.S., Li G., Luo M.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY216659; AAC60104.1; -
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
DR SEQUENCE 418 AA; 46465 MW; 5CTCAFBD519980F CRC64;

Query Match 83.9%; Score 1788; DB 11; Length 418;
Best Local Similarity 83.2%; Pred. No. 3.5e-131;
Matches 347; Conservative 37; Mismatches 23; Indels 4; Gaps 3;

QY 1 MQALVLLICIGALLGHSSCON--PASPPPEGSDPDSTGALVEBEDPFFKVPVKNKLAASV 58
DB 1 MQTLVLLWTGALLGHSSQNVPS--SQDSPAPDSTGEPVEEDPFFKVPVKNKLAASV 58

QY 59 SNFGYDLVVRSSMPTTNVLLSPLSVATALSALSGAEQRTESIIRALYYDLITSPDI 118
DB 59 SNFGYDLVRLSSASPTGNVLLSPLSVATALSALSGAEHRTESIIRALYYDLITNPDI 118

QY 119 HCTYKELDTVTAPQKNLKSASRIIVFEKLRKKSFPVAPLEKSYGTRPRVLTGNPRDLQ 178
DB 119 HSTYKELLASVTAPKKNLKSASRIIVFEKLRKKSFPVAPLEKSYGTRPRILTGNPRDLQ 178

QY 179 EINNVOQOMKGLARSTKEIPDEISILLGVAFKQGWTKFDSRKTSLDFVLDERTV 238

QY 360 AGFENWEDGAGTTSPGLQPAHLTFPLDYHLNQPFIFVLRDRTDTGALLFGKILDP 415
DB 359 AAFENWEGAGSSPGLQPVRLTFPLDYHLNQPFIFVLRDRTDTGALLFGKILDP 414

RESULT 2
Q88691 PRELIMINARY; PRT; 417 AA.
ID Q88691
AC Q88691
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Capsin.
GN SERPINP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=98279032; PubMed=9614124;
RA Kozaki K., Miyashita O., Koike O., Yasui Y., Kashiwai A.;
RA Nishikawa Y., Shimizu S., Suga S.;
RT "Isolation, purification and characterization of a collagen-associated
RT serpin, caspin, produced by murine colon adenocarcinoma cells.";
RL J. Biol. Chem. 273:15125-15130(1998).
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; D87975; BAA31978.1; -
DR HSSP; P36955; 11MW.
DR MGD; MGI:108080; Serpin1.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Protease inhibitor; Serine protease inhibitor; Serpin.
SQ SEQUENCE 417 AA; 46220 MW; ADD224FA2BA51A00 CRC64;

Query Match 86.9%; Score 1851.5; DB 11; Length 417;
Best Local Similarity 86.3%; Pred. No. 3.9e-136;
Matches 359; Conservative 34; Mismatches 20; Indels 3; Gaps 2;


```
Db 179 EINNVOAQMGKARSTREMPALSILLGVAVFKQWATKFSRKTTLQDFHLEDRT 238
Qy 239 VRVPMSPDKAVLRGLDSDLSCKIAQLPTGSMIIFFFLPKVTQNLTLIEESLTSEFI 298
Db 239 VRVPMSPDKAVLRGLDSDLSCKIAQLPTGSMIIFFFLPKVTQNLTLIEESLTSEFV 298
Qy 299 HDIDRELTQVAVLTVPKLSYGEVTKSLQEMKLSLDFSPDFSKITGPKLQVH 358
Db 299 HDIDRELTQVAVLTVPKLSYGEVTKSLQEMKLSLDFSPDFSKITGPKLQVH 358
Qy 359 RAGEWNEEDGAGTTPSGLOPAHLTFPLDYLHNOPIFVLRTDTGALLFGKILDP 415
Db 359 RAGEWNEEDGAGTTPSGLOPAHLTFPLDYLHNOPIFVLRTDTGALLFGKILDP 415

RESULT 4
Q13236 PRELIMINARY; PRT; 362 AA.
AC Q13236;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Pigment epithelium-derived factor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tombran-Tink, J., Mazuruk, K., Rodriguez I., Kouri R.E., Chung D.,
RA Linker T., Chader G.J.;
RT "Cloning and molecular characterization of the human gene for the
RT neurotrophic serpin PEDF: conservation, polymorphism and hereditary
RT studies."
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; U29953; AA084914.1; -.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR HSP; P36955; 11MV.
DR InterPro: IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
KW Protease inhibitor; Serine protease inhibitor; Serpin.
SQ SEQUENCE 362 AA; 40071 MW; 650E4C63767B54DD CRC64;

Query Match 83.7%; Score 1784; DB 4; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.8e-131; Indels 0; Gaps 0;
Matches 358; Conservative 0; Mismatches 0;

Qy 1 MQALVLLCIGALGHSSCONPASPPEGSPDPDSTGALVEEDPFFKVPVKNKLAASVN 60
Db 1 MQALVLLCIGALGHSSCONPASPPEGSPDPDSTGALVEEDPFFKVPVKNKLAASVN 60
Qy 61 FGVDLYVRSMSPTTNVLSPVATLSALSGAEQRTESIHRALYDLISSPDHIG 120
Db 61 FGVDLYVRSMSPTTNVLSPVATLSALSGAEQRTESIHRALYDLISSPDHIG 120
Qy 121 TYKELLDTVAPQKNLKSASRIVEKKLRKIKSFVAPLEKSYGTRPRVLTGNPRLDLQEI 180
Db 121 TYKELLDTVAPQKNLKSASRIVEKKLRKIKSFVAPLEKSYGTRPRVLTGNPRLDLQEI 180
Qy 181 NNWVQAMKGLARSTKEIPEISILLGVAVFKQWATKFSRKTSLIEDERTVTR 240
Db 181 NNWVQAMKGLARSTKEIPEISILLGVAVFKQWATKFSRKTSLIEDERTVTR 240
Qy 241 VPMMSDPKAVLRGLDSDLSCKIAQLPTGSMIIFFFLPKVTQNLTLIEESLTSEFIHD 300
Db 241 VPMMSDPKAVLRGLDSDLSCKIAQLPTGSMIIFFFLPKVTQNLTLIEESLTSEFIHD 300
Qy 301 IDRELKTVQAVLTVPKLSYGEVTKSLQEMKLSLDFSPDFSKITGPKIKLTQ 355
Db 301 IDRELKTVQAVLTVPKLSYGEVTKSLQEMKLSLDFSPDFSKITGPKIKLTQ 355
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RESULT 5
Q42453 PRELIMINARY; PRT; 448 AA.
AC Q42453;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Serpin precursor.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OC NCBI_TaxID=7757;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Larval liver;
RA Robson P., Li F., Youson J.H., Keeley F.W.;
RT "Identification and characterization of a serpin with differential
RT expression during the life cycle of the sea lamprey,"
RL Comp. Biochem. Physiol. B, Comp. Biochem. 120:253-263 (1998).
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; AF009964; AAC63406.1; -.
DR HSP; P01012; IOVA.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro: IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Protease inhibitor; Serine protease inhibitor; Serpin; Signal.
FT SIGNAL 1 21
FT CHAIN 22 448
SQ SEQUENCE 448 AA; 49044 MW; 5F925AC1B45PDEF9 CRC64;

Query Match 25.2%; Score 537; DB 13; Length 448;
Best Local Similarity 29.6%; Pred. No. 2e-33;
Matches 123; Conservative 91; Mismatches 183; Indels 18; Gaps 6;

Qy 4 LVLLCIGALGHSSCONPASPPEGSPDPDSTGALVEEDPFFKVPVKNKLAASVNFQY 63
Db 12 LVTLISLG-FADHGHGTFGAPPV-----SATAI-----SPV---VSRLAGSQGDFGF 56
Qy 64 DLYVRSMSPTTNVLSPVATLSALSGAEQRTESIHRALYDLISSPDHIGTYK 123
Db 57 QFFHKLGEASPGQNVLFSPPLTSAALMLLAGSGDKTQLTNALRLQFLRDPNPAQSFQ 116
Qy 124 ELLDVTAPQKNLKSASRIVEKKLRKIKSFVAPLEKSYGTRPRVLTGNPRLDLQEI 183
Db 117 ALVSKLHGRDSTNTAARIFTAKHATIKQQLDAVEKYKAKPKQLIGNMKEDVALINKW 176
Qy 184 VQAMKGLARSTKEIPEISILLGVAVFKQWATKFSRKTSLIEDERTVTRVPM 243
Db 177 VAEKTEGHIIDPVKELPEELQLFIVSAIFFKQKWLKPFQVESTSPRPHLSPNETQVPT 236
Qy 244 MSDPKAVLRGLDSDLSCKIAQLPTGSMIIFFFLPKVTQNLTLIEESLTSEFIHD 303
Db 237 MFASGYPKKGHPSPVTVAKIQGNTSLLLFFVDVAVSTNLSALESSQLVTLVE 296
Qy 304 ELKTVQAV-LTVPKLKSVEGEVTKSLQEMKLSLDFSPDFSKITGPKIKLTQVHRA 362
Db 297 ETLVQKKTDLVPLSLDVSNEIEQLTDIGLDLFTKPTDLSKISDIPRYSKVHRA 356
Qy 363 ENNEGAGTTPSGLOPAHLTFPLDYHL--NOPFFVLRTDTGALLFGKILDP 415
Db 357 TLNEEGVKATAATGIMISLMSVQHSSEELKVDPRPFVLIRDDDETGALLFVGRVTP 411

RESULT 6
Q8NSU7 PRELIMINARY; PRT; 491 AA.
AC Q8NSU7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
```

01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DT Hypothetical protein.
 DE Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon, and Kidney;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: AAH31592.1;
 DR EMBL; BC031592; AAH31592.1;
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
 DR InterPro: IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SMO0093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 DR Hypothetical protein; Protease inhibitor; Serine protease inhibitor;
 KW Serpin.
 SQ SEQUENCE 491 AA; 54593 MW; 9CCF5B1D21C6E03 CRC64;
 Query Match 21.48; Score 456.5; DB 4; Length 491;
 Best Local Similarity 28.44; Pred. No. 4.5e-27;
 Matches 127; Conservative 86; Mismatches 181; Indels 53; Gaps 11;
 QY 5 VLLICIGALLGHSCQNPAS-----PPEE-----GSPDPSTGAL--- 39
 DB 7 LLVLSWCLQPCGVSVSAMRGLRQLTSGFNQEQVSLTLKLGNEPQGQATKSP 66
 QY 40 --VEEDDPFKVP--VNKLAAVSNFGYDLYRVSSMPTNVLSPVATLSLSLG 95
 DB 67 PGVCSRDP---TPEQTHRLARMAFAFTADLSVAQTSTCPNLISPLSVALLSHLAG 123
 QY 96 AE-----RTESIHRALYDILSSPDHGTGYKYLITDTVTAPOXNLKSASRIPEKRLK 151
 DB 124 AQNHTLQRLQVLAG-----SGPCLPHLLSLRQLDQGLPGAFRL--AARMYLQKFPK 175
 QY 152 SSFVAPLEKSYGTRPRVLVTGNPLRDLQEIINNVOAQMKGKLARSTKEIDETISILLGVA 211
 DB 176 EDFLEQSEQLFGAKFVSLTKQEDDLANINQWKEATEGKIQBFSLGSLPDTVLLILNAI 235
 QY 212 HFKGQWTKDSRSTSLDFYLBERTVVRVPMKSDPKAVLYRGLDLSCKLAQLPTGS 271
 DB 236 HFQGFWRNKDPSLTQRDSFHLDEQFTVPMQARTYPLRWFLLEQPEIQVAHFPPKN 295
 QY 272 MSIIFFPLKVTQNTLIEESLTSEFIHD---IDRELKTVOAVLTVPKLSYEGEVTKS 328
 DB 296 MSFVLVPTHFEMVNSQVLANSLWDTLHPLVWERPTK-----VRLPKLYLKHQMDLVAT 350
 QY 329 LOEMKLSLSDSPDFSKITGPKIKLTOVEHRAGFENEDGAGTTPSPGLQPAHLTFPLDY 388
 DB 351 LSQGLQELFQAPDLRGISQSLVVGQHQSTLEUSEVGVEAAATSIAMSRNSLS-SF 409
 QY 389 HLNOPFIFVLRTDTGALLFTGKILDP 415
 DB 410 SVNRPFLLFFEDTGLPLFVGSRNP 436
 RESULT 7
 ID Q80X76 PRELIMINARY; PRT; 471 AA.
 AC Q80X76;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE LOC238393 protein (fragment).
 GN LOC238393.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Salivary gland;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
 RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;
 RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;
 RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Heieh F.;
 RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
 RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
 RA Rana S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullaby S.J.;
 RA Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gumarane P.H.;
 RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;
 RA Villalón D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
 RA Fahey J.; Helton E.; Kettman M.; Madan A.; Rodriguez S.; Sanchez A.;
 RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;
 RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
 RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.;
 RA Krzywinski M.I.; Skalska U.; Smallos D.B.; Scherch A.; Schein J.E.;
 RA Jones S.J.; Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Salivary gland;
 RA Strausberg R.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC049975; AAH49975.1;
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
 DR InterPro: IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SMO0093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 FT NON TER 1
 SQ SEQUENCE 471 AA; 52756 MW; 482DB301DB9D8BEA CRC64;
 Query Match 21.34; Score 453; DB 11; Length 471;
 Best Local Similarity 30.14; Pred. No. 7.9e-27;
 Matches 123; Conservative 81; Mismatches 184; Indels 20; Gaps 10;
 QY 24 SPPEEGSDPP--DSTGALVEEDPFFKVPVNKLAAVSNFGYDLYRVSSMPTNVLSS 81
 DB 31 SPVFGCPDVLGRNTAVREVENITSDVSLTASSNTDFAFSLYKELVKNPDENVVFS 90
 QY 82 PLSVATLSALSIGAEQRTESIHRALYDILSS--PDHCTYKELDTVTAP--OKNLK 137
 DB 91 PFSICTALTLSLGAKNLTKLELGKLFNLTETPEPDHGGFRYLLDLSSQPNQVCIS 150
 QY 138 SASRIVFEKKLRIRKSSFVAPLEKSYGTRPRVLVTGNPELDLQE---INNVOAQMKGKLAR 194
 DB 151 TGSALFIEKHQILAEFEKARALY--QAFAFTADFOQPLEATKLINDYVSNQTOGKKE 208
 QY 195 STKEIPDEISILLGVAFHFGQWTKFDSRSTSLDFYLBERTVVRVPMKSDPKAVLYRG 254
 DB 209 LISDLKRTLMVLVNIYFKGKWEPPDPDDTCKSEFYLDENRSVKVPMKINNLTPPYF 269
 QY 255 LDSLSCKIAQPLTGTSMISIFFPLKVTQNTLIEESLTSEFIHDIDRELK-TVQAVLT 313
 DB 269 RDELSCTVVELKVTGNASAFILPDQ--GKQQQVEASLQPELTKNNKWSLKPRLIDELC 326
 QY 314 VPKLSYEGEVTKSLQMKLSQSLFDS--PDFSKITG-KPKILTOVEHRAGFENEDGAGT 371
 DB 327 LPKFSISTDYSLEHILPELGRLEFSTQADLSAITGTKDLRTSQVHVHKAVIDVAETGEA 386
 QY 372 TSPSGLOPAH---LTPLDYLHNPPIFVLRTDTGALLFTGKILDP 415
 DB 387 AAGTGYNLQCCQGVISGKTYFDRPFLMIISDNTIHIALFMKAVTNP 434
 RESULT 8
 Q60552
 ID Q60552 PRELIMINARY; PRT; 420 AA.

AC Q60552;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Pregnancy protein 60 kDa precursor.
GN HPP.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Waterhouse; TISSUE=Liver;
EA Park C.G.;
RT "Cloning and sequencing of a new pregnancy marker protein from hamster
liver";
RT Thesis (1992), Biological Sciences, The Wichita State University.
RL -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC EMBL; M96650; AAA37078.1; -.
DR HSSP; P01011; 1A54.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Protease inhibitor; Serine protease inhibitor; Serpin; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 420 PREGNANCY PROTEIN 60 KDA.
FT SEQUENCE 420 AA; 47490 MW; 3B9859D19A34EFA CRC64;
Query Match 20.7%; Score 441.5; DB 11; Length 420;
Best Local Similarity 28.0%; Pred. No. 5.3e-26;
Matches 123; Conservative 90; Mismatches 175; Indels 51; Gaps 11;
QY 4 LVLLCTGALLGSSQCPSPPEGSPDPSTGALVEEDPFFKVPVKNKLAAYSN--F 61
DB 5 VAFILLVAAPCPAVLC-----QDGLTKETT--VOEQNKETKVDLSLTASINTDFAF 56
QY 64 DLVVRSSMPTTNVLLSPLSVATLSALSLGAEQRTESIHRALYYDLTSSP--DIHG 121
DB 57 SLYKQALKKPKDKVIFSPFSISFALAFSLGASSNTLEILGLKENLTETPEALH 116
QY 122 YKELDTVTAP--QKNLKSASRIVFEKLRKISFVAPLEKSYGTGTRPVLTGNPRLD 179
DB 117 FGHLLRLMSOPGQGVSTSSAMEVEKRLQLAEFFKKARALYCAEA-----S 170
QY 180 -----INNVAQMKGLARSTKEIPDEISILLGVAFHKGQVTKPDSRKTSL 232
DB 171 PHEAKKLINDYVSKTHGKIKELMSDDDDQTSWLVNVIYFKGKWKAPFPDFTY 230
QY 233 LDEERTVVRPMSPDKAVRLYGLDSDLCKIAQLPLTGSMSIIFFLPK-----V 282
DB 231 LDNKRKVKVPMKHKDLTPYFRDEELSSYVVMRYGNVSAMFILPKGRMQQL 290
QY 283 TQNTLLEESLTSFFIHIDRELKTVQAVLTVPKLSYGEVTKSLQEMKLSLQ 341
DB 291 PETLRWKDLSLRPMIHE-----LYVPKFSISTDYSIEGLSQIGKEVFSSQA 339
QY 342 DFSKITG-KPKLTQVEHRAAGFENWEDGAGTTPSPGLQ---PAHLTPFLDYHLNQ 397
DB 340 DLSGITGDKLRVSKVVKHKAVDLGVETGTEAAATGLRMVGSALINPLRKNKFLMI 399
QY 398 LRDTDTGALLPFGIKLDP 416
DB 400 IYNTNTQTLFMAKVTNPK 418
RESULT 9
ID Q9GMA6 PRELIMINARY; PRT; 415 AA.
AC Q9GMA6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
GN AACT2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9923;
RN [1]
RP SEQUENCE FROM N.A.
RC Stratil A.; Peelman L.; Mattheeuws M.;
RT "The porcine alpha-1-antichymotrypsin 2 (AACT2) gene: nucleotide
sequence, genomic organization and polymorphism";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBSJ databases.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; AJ297654; CAC05490.1; -.
DR HSSP; P01011; 1A54.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Protease inhibitor; Serine protease inhibitor; Serpin; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 415 ALPHA-1-ANTICHYMOTRYPSIN 2.
FT VARIANT 399 399 I -> V.
FT VARIANT 401 401 K -> N.
FT SEQUENCE 415 AA; 46645 MW; EF29767E63D59060 CRC64;
Query Match 20.2%; Score 429.5; DB 6; Length 415;
Best Local Similarity 28.3%; Pred. No. 4.5e-25;
Matches 121; Conservative 87; Mismatches 188; Indels 31; Gaps 11;
QY 4 LVLLCTGALLGSSQCPSPPEGSPDPSTGALVEEDPFFKVPVKNKLAAYSN--F 61
DB 5 LALGLLVAGLCRVEHC-----VPADDPASKIVTLKQIKKLPAHNTAVVSSNTDF 54
QY 62 GYDLVVRSSMPTTNVLLSPLSVATLSALSLGAEQRTESIHRALYYDLTSSP--DIH 119
DB 55 AFSLYKQLALTNPHENVIFSPLSVSMALAFSLGARGPTLTLEGLAKFNLTKTPEABI 114
QY 120 GYKELDTVTAPQK--NLKSASRIVFEKLRKISFVAPLEKSY-----GTRPVLTGN 172
DB 115 QCFQHLSTLDRSSNLLQLRLGNAMFIDEQLELDKFKVQDAHELYHSEAFPTNFDLEAA 174
QY 173 PRLDQLQENNVQAQMKGLARSTKEIPDEISILLGVAFHKGQVTKPDSRKTSL 232
DB 175 RL-----INDYVKNTEGKIVDLFKKLDPLKVLVNVVIYFKAKWKTFFNPLTTEAD 230
QY 233 LDEERTVVRPMSPDKAVRLYGLDSDLCKIAQLPLTGSMSIIFFLPKVTQNTL 292
DB 231 VSKNRTVVRPMGIRALTVPYFRDEELACTVVELFPTSNDLSALFLP--DGRMAAVEAK 288
QY 293 LTSEFIHIDRELKTVQAV-LTVPKLSYGEVTKSLQEMKLSLQ 349
DB 289 LPETLRWRDLPQRPWIVELYLPKFSISSDVRULHEILPQGLIEIFGNANLSITWK 348
QY 350 PIKLTQVEHRAAGFENWEDGAGTTPSPGLQ--PAHLTPFLDYHLNQPFIVLRD 408
DB 349 PLKVSGVHSAVLDVNEEGTEAAATGIDINVRSLERIALHFNRPFLFVIISKDIQSI 408
QY 409 ICKILDP 415
DB 409 LGKVTKP 415
RESULT 10
ID Q8VCH3 PRELIMINARY; PRT; 418 AA.
AC Q8VCH3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Serine protease inhibitor 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; BC019802; AAH19802.1; -.
DR HSP; P01009; IOLP.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Protease; Protease inhibitor; Serine protease inhibitor; Serpin.
SQ SEQUENCE 418 AA; 46851 MW; DF5DC0362F3A291 CRC64;
Query Match 19.8%; Score 421; DB 11; Length 418;
Best Local Similarity 30.9%; Pred. No. 2.1e-24;
Matches 118; Conservative 80; Mismatches 154; Indels 30; Gaps 12;
Y 54 LAAAVSFGDYLVRRSSMPTTNVLLSPVATLSALSLGAEQRTESIIRHLYYDLI 113
D 48 LASVNTDFAFSLYKALKKPNPTNIVFSPUSISAAALVSLGAKGTMBEILGLKFNLT 107
Y 114 SSP--DIHGTYKELLDTVTAP--QKNLKSASRIVFEKRLKIKSFVAPLEKSYGTRPRVL 169
D 108 ETPEADTHQGFGLNLSQSPEDQDQINIGNAMFIEKDLQILAEF---HEK---TRALYQ 161
Y 170 TGNPRLDQ-----INNVOAQMGKGLARSTKEIPDEISILLGLVAHFKGOWTKFD 222
D 162 TEAFTADFPQTEAKNLINDYVSNQTMKELISELDETRTLMVLVNYIYFKGKWKISFD 221
Y 223 SRKTSLEDFYLDERTVVRPMSPDKAVLYRGDLSCKIAQLPLTSGMSIIFFLPKV 282
D 222 PQDFESEFYLDKRSVKVPMKMLTTRHFRDEELSCVLELKYTGNASALLILPDQ- 280
Y 283 TQNTLTLESITSEFIHIDRELKTQV-AVLTVPKLKLSEGEVTKS-LOEMKLSLF-D 339
D 281 -GRMQQVEASLPQTELRKWKRTLPFSQIEELNLPKFSIASNYRLEEDVLPENGKVFTE 339
Y 340 SPDSKIT-GKPIKLTQVEHRAGFENEDG---AGTTPSPGLQPAHLTPPLDYHLNQPF 394
D 340 QADLSGITETKLSVSVQVHKAVLDVAETGTEAAATGVIGGIRKAILP---GVHFNRRF 396
Y 395 IFVLRDQDTGALLFIGKILDP 416
D 397 LFVIYHTSAQSILFMKVNPK 418
RESULT 11
ID Q91X80 PRELIMINARY; PRT; 418 AA.
AC Q91X80;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Serine protease inhibitor 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

DR EMBL; BC011217; AAH11217.1; -.
DR HSP; P01009; IOLP.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Protease; Protease inhibitor; Serine protease inhibitor; Serpin.
SQ SEQUENCE 418 AA; 46866 MW; DF5DC0362F5C2F7 CRC64;
Query Match 19.7%; Score 420; DB 11; Length 418;
Best Local Similarity 30.9%; Pred. No. 2.5e-24;
Matches 118; Conservative 80; Mismatches 154; Indels 30; Gaps 12;
Y 54 LAAAVSFGDYLVRRSSMPTTNVLLSPVATLSALSLGAEQRTESIIRHLYYDLI 113
D 48 LASVNTDFAFSLYKALKKPNPTNIVFSPUSISAAALVSLGAKGTMBEILGLKFNLT 107
Y 114 SSP--DIHGTYKELLDTVTAP--QKNLKSASRIVFEKRLKIKSFVAPLEKSYGTRPRVL 169
D 108 ETPEADTHQGFGLNLSQSPEDQDQINIGNAMFIEKDLQILAEF---HEK---TRALYQ 161
Y 170 TGNPRLDQ-----INNVOAQMGKGLARSTKEIPDEISILLGLVAHFKGOWTKFD 222
D 162 TEAFTADFPQTEAKNLINDYVSNQTMKELISELDETRTLMVLVNYIYFKGKWKISFD 221
Y 223 SRKTSLEDFYLDERTVVRPMSPDKAVLYRGDLSCKIAQLPLTSGMSIIFFLPKV 282
D 222 PQDFESEFYLDKRSVKVPMKMLTTRHFRDEELSCVLELKYTGNASALLILPDQ- 280
Y 283 TQNTLTLESITSEFIHIDRELKTQV-AVLTVPKLKLSEGEVTKS-LOEMKLSLF-D 339
D 281 -GRMQQVEASLPQTELRKWKRTLPFSQIEELNLPKFSIASNYRLEEDVLPENGKVFTE 339
Y 340 SPDSKIT-GKPIKLTQVEHRAGFENEDG---AGTTPSPGLQPAHLTPPLDYHLNQPF 394
D 340 QADLSGITETKLSVSVQVHKAVLDVAETGTEAAATGVIGGIRKAILP---AVHFNRRF 396
Y 395 IFVLRDQDTGALLFIGKILDP 416
D 397 LFVIYHTSAQSILFMKVNPK 418
RESULT 12
ID Q03734 PRELIMINARY; PRT; 418 AA.
AC Q03734;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Contrapsin related protein (Similar to serine protease inhibitor-2 related sequence 1) (Serine (or cysteine) proteinase inhibitor, clade A, member 3M).
GN SERPINA3M OR SP12-RS1 OR CMC7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Ohkubo K., Ogata S., Misumi Y., Takami N., Sinohara H., Ikahara Y.;
RT "Cloning, structure, and expression of mouse contrapsin and its related protein.";
RL Biochem. J. 0:0-0(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner I., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marta M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR ENBL; X53148; CAA39949.1; -.
 DR ENBL; BC011158; AAH11158.1; -.
 DR ENBL; BC053337; AAH53337.1; -.
 DR PIR; S23675; S23675.
 DR HSP; P01011; 2ACH.
 DR MGD; MGI:98378; Serpina3m.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 KW Protease; Protease inhibitor; Serine protease inhibitor; Serpin.
 SQ SEQUENCE 418 AA; 47004 MW; 32D957F693D69B79 CRC64;
 Query Match 19.6%; Score 418; DB 11; Length 418;
 Best Local Similarity 28.8%; Pred. No. 3.6e-24;
 Matches 119; Conservative 75; Mismatches 165; Indels 54; Gaps 11;
 QY 27 EGSPDPSICALVEEDPEKYPVNKLAASVNGFDLYVRSSMPTNVLSPLSVA 86
 Db 37 ESGTPDPSLT-----LASINTDFAPSLYKELVLKPNPKNIVFSPLSIS 79
 QY 87 TALSALSLGAEQRTESIIRALYYDL--ISSPDHGTYYKELDTVTAP--QKNLKSASRI 142
 Db 80 AALALVSLGAKNTLEILEGLKFNLTETSEADHQFGHLLQRLSQPEDQDQINIGNAM 139
 QY 143 VFEKLRKISFVAPLEKSGTGRPRVTGNPRDLQE-----INNVOAQMKGLARS 195
 Db 140 FIEKDLQILAEFHEKARALYQTEFT-----ADFQKTEAKNLINDYVSNQTQMIKEL 193
 QY 196 TKEIPDPSIILLGVAFKQGWTKFDSRKTSLDFLDERTVRYPMMSDPKAVLRYGL 255
 Db 194 ISELDLTLMLVNVNIVFKGKWKISPDQTFSEFVLEKRSVKVPMKMKELTTRHFR 253
 QY 256 DSDLSCKIAQLPTGNSMIIFFPLKVTQNLTLIESLTSFTHIDRELKTVQ-AVLTV 314
 Db 254 DEELSCSVLELKYTGASALFILPDQ--GRMQVEASLQPETLRKWKWSLKTKIGELYL 311
 QY 315 PKLKLISYEGEWTSLQMKLQSLFD-SPDFSKITG-KPIKLTOVEHRAGFENNEDGAGIT 372
 Db 312 PKFSISTDYNLKKDILPELGRKELFSGKQADLSGTGINKLQSVQVHKAULDVAGTETAA 371
 QY 373 PSPG-----LQPAHLTFPLDYHLNPPFIIVLRDRTDTGALLFICKILDR 416

Db 372 AATGFIQFGRSRLQTMVTQVF-----NRPFLMVISHTGVQTTLFMAKVTNPK 418
 RESULT 13
 P97569
 ID P97569 PRELIMINARY; PRT; 423 AA.
 AC P97569;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Kallistatin.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Chai K.X., Ni A., Chen V.C., Lindpaintner K., Rubattu S., Chao J.,
 RA Chao L.;
 RT "Molecular cloning and characterization of the rat kallistatin gene.";
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR ENBL; U51017; AAB39509.1; -.
 DR HSP; P01011; 1AS4.
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 KW Protease inhibitor; Serine protease inhibitor; Serpin.
 SQ SEQUENCE 423 AA; 48021 MW; 133456709BDB2FE9 CRC64;
 Query Match 19.6%; Score 418; DB 11; Length 423;
 Best Local Similarity 28.3%; Pred. No. 3.6e-24;
 Matches 122; Conservative 94; Mismatches 179; Indels 36; Gaps 14;
 QY 5 VLLLCIGAL-IGHSSCQNPASPPERGSDPDSTGALVEEDPFFKVPVNKLAASVNGFY 63
 Db 7 LLLLAGLELHSHS-----QPDQE--EPDNTNTQYRQFSQQNISSYQIASGNAPAF 57
 QY 64 DLYVRSSMPTNVLSPLSVATLSALSGAEQRTESIIRALYYDL--ISSPDHGT 121
 Db 58 RLYHLIASQNSEKNIFSPISVSLSAILSTGAGDQAOILLEGFLNLTLSLPEIHG 117
 QY 122 KYELDTVTAP--QKNLKSASRIPEKLRJIKSSVAPLEKSYGTRPVLTGNPR--LD 176
 Db 118 FSLQHTIARPTPEQISVSGALILSLQNLSEFVSAIETSYNS--KVLHANFRDKAA 175
 QY 177 LQEIINNVOAQMKGLARSTKEIPDEISILLGVAFKQGWTKFDSRKTSLDFYLD 236
 Db 176 VOLINNYYKQNTQGIKNLVSDLSDPDKVNLVNIYFFQGLWKPKPPFSRVSTSDYVD 235
 QY 237 RTVRYPMMSDPKAVLRYGLDSDLSCKIAQLPTGNSMIIFFPLKVTQNLTLIESL 296
 Db 236 TVVKIPMKLQDKEDHWHLEDRRVPCTVLRMDYRGDAVAFILPDQGN--EVEQVLS 293
 QY 297 FTHIDRELKT----VQAVLTVPKLSYEGEWTSLQMKLQSLF-DSPDFSKITGK-P 350
 Db 294 MLLRWKRLQNRFYFKLILQLPKFSISNSYELDELPLDGLQDLFTENANFSNISK 353
 QY 351 IKLTOVEHRAGFENNEDGAGITPSGLQPAHLTF-----PLDYHL--NOPFFVL 404
 Db 354 LYLKVFVFKTKVLDVNVNEVTKAAATG---SPATFSAQPKKRYLIFNRPFLVILY 410
 QY 405 ALLFTGKILDP 415
 Db 411 DILFKGVNVP 421
 PRELIMINARY; PRT; 406 AA.
 RESULT 14
 Q64118
 ID Q64118 PRELIMINARY; PRT; 406 AA.

AC Q64118;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Alpha-1-antitrypsinase.
 DB Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
 OC Meriones.
 OK NCBI_TaxID=10047;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=9515526; PubMed=7852275;
 RX Goto K., Suzuki Y., Yoshida K., Yamamoto K., Sinchara H.;
 RT "Plasma, alpha-1-antitrypsinase from the Mongolian gerbil, Meriones
 unguiculatus: isolation, partial characterization, sequencing of cDNA,
 RT and implications for molecular evolution.";
 RL J. Biochem. 116:582-589 (1994).
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR EMBL; S77822; AAB33367.1; -;
 DR PIR; JX0346; JX0346.
 DR HSSP; P01009; IQLP.
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 DR Protease; Protease inhibitor; Serine protease inhibitor; Serpin.
 KW SEQUENCE 406 AA; 45126 MW; 814613E44C7AA469 CRC64;
 SQ
 Query Match 19.6%; Score 417; DB 11; Length 406;
 Best Local Similarity 30.0%; Pred. No. 4.1e-24;
 Matches 114; Conservative 83; Mismatches 151; Indels 32; Gaps 11;
 QY 54 LAAVSNFGDYVRSMPTTNVLSPLSVATLSALSLGAEQRTESIHRALYIDL- 112
 DB 39 MASNLDAFAGLYVLSHQSNNTNIFLSPLSIATLAMLGLSGKDDTKAQLLOGLHFNLT 98
 QY 113 -ISSPDHGYKELDTVTPAQVNLK--SASRVFEKKLRKISFVAPLEKSYGTRPRVL 169
 DB 99 ETSEADIKGFQHLKLTNRPNDELQLTGSSLFVNNSLNLVEKFLVEEVKNHYHSEAFFV 158
 QY 170 TGNPRLDQE----INNVAQAKGLARSTKIPDEISILLGVAFHKGQWTKDSRK 225
 DB 159 N---FASSEAKTINFEVEKATGKIVDLVVKLEIDTVLALVNYIFFRGKWEKPDPEL 215
 QY 226 TSLEDFYLDERTVVRVPMSPDKAVLYGL-----DSDLCKIAQPLTGSMSIIFFLPL 280
 DB 216 TEEADFHVDKSTTVKVPWN-----RMGMFVHYCDTLSSWVLLMDYLGNAIAIFILPD 269
 QY 281 KVTQNLTLIEBSLTSETHIDRELKTVQAVLTVPKLKSVEGEVTKSLQEMKLSLF-D 339
 DB 270 E--GKQHLQTLTKHEIYKFLQNRHTRSANVHLPLKLSISGTYNLKLVSLGITQVFN 327
 QY 340 SPDFSKI--TGKPIKLTQVEHRAGFEMNEDG---AGTTPSPGLQPAHLTPPLDYHLNQPT 395
 DB 328 GADLSGITDVPKLSKXAVHKAULTDERTGAAGTTV---LEAVPMSIPDVCFKNPFV 384
 QY 396 FVLDDTDGALLFGKILDP 415
 DB 385 VIICKRHTQSPFLVGVKNP 404

RESULT 15

Q91WP6

ID Q91WP6

AC Q91WP6

DT 01-DEC-2001

DT 01-DEC-2001

DT 01-DEC-2001

DT 01-JUN-2003

DE Serine protease inhibitor 2-2.

CN SERPINA3N

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=Liver;
 RA Strausberg R.;
 RL Submitted (SSP-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR EMBL; BC013651; AAH13651.1; -;
 DR HSSP; P01009; IQLP.
 DR MGI; MGI:105045; Serpina3n.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 DR Protease; Protease inhibitor; Serine protease inhibitor; Serpin.
 KW SEQUENCE 418 AA; 46718 MW; 4BF21BBE10A91F6C CRC64;
 SQ
 Query Match 19.5%; Score 416.5; DB 11; Length 418;
 Best Local Similarity 28.7%; Pred. No. 4.7e-24;
 Matches 115; Conservative 85; Mismatches 180; Indels 21; Gaps 10;
 QY 33 PDST----GALVEEDPFFKVPVKNKLAANVSNFGDYLRVRSMSPTNVLLSPLSVATA 88
 DB 22 PDGTGLMDAAVQEDHDNGTQDLSLTLASINTDFASLYKELVLKPNKINIVFSPLSISAA 81
 QY 89 LSALSGLGAEQRTESIHRALYIDL--ISSPDHGYKELDTVTPAQVNLK--SASRVFE 144
 DB 82 LAVMSLGAAGNTLSEILEGLKFNLTETSEADIHQGFGLHQLRLNQPKDQVISTGSAFLI 141
 QY 145 EKKURIKSFVAPLEKSYGTRPRVLN---PRLDQEIINNVAQAKGLARSTKIPD 201
 DB 142 EKRQILTFEFOEKATLY--QAEAFADFOQROAKKLINDYVRKOTQGMIKELVSLDK 199
 QY 202 EISILLGVAFHKGQWTKFDSRXTSLEDYLDERTVVRVPMSPDKAVLYRGLDLSLSC 261
 DB 200 RLVVLYVNYIYFKAKWKVFPDPLDTFKSEFVAGKRRPVIVPMMSMEDLTTPYFRDELSLSC 259
 QY 262 KIAQLPLTGSMSIIFFLPKVTONLTIEBSLTSETHIDRELK--TVQAVLTVPKLKS 320
 DB 260 TVVELKVTGNASALFILPDQ--GRMQQVEASLOPETLRKWNKNSLXPRMIDELHLPKFSIS 317
 QY 321 YEGEVTKSLQEMKLSLQSLFDS--PDFSKITG--KPIKLTQVEHRAGFEMNEDGAGTTPSPGLQ 378
 DB 318 TDYSLEDVLSKLGIREVFSTQADLSAITGTDLRVSVQVHVHKAULTDERTGAAGTTV--- 377
 QY 379 PAHLT---FPLDYHLNQPTFVLRDITDTGALLFGKILDP 416
 DB 378 FVPMKAKLYPLTVVFNRPFLIMIFDTETETIAFFAKIANPK 418
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 Job time : 124 secs